98851

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SEARCH REQUEST FORM

Scientific and Technical Inf rmation Center

Requester's Full Name: Gary Counts Examiner #: 78696 Date: 7/15/03
Art Unit: 1641 Phone Number 30 5-1444 Serial Number: 09/923716
Mail Box and Bldg/Room Location: CM1 7D16 Results Format Preferred (circle): PAPER DISK E-MAIL
mail Box : 7E12
If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Process for detecting serine/threonine Kinase activity

Inventors (please provide full names): Joachim Kramer, Thomas Mander, Richard Bethell
Neil Benson

Earliest Priority Filing Date: 8/11/2000

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search

Claim 10 - Seq I.D NO: 4 11

Claim 15 Seq ID NO: 2 11

claim 16 SeQ ID NO: 1 11

all NAs

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Date Searcher Picked Up: 7/16
Date Completed: 7/17
Searcher Prep & Review Time: 5
Clerical Prep Time: 4
Online Time: 10

Type of Search

NA Sequence (#) B
AA Sequence (#) 3
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
Dialog _____
Questel/Orbit _____
Dr.Link _____
Lexis/Nexis _____
Sequence Systems OR
WWW/Internet _____
Other (specify) _____

PTO-1590 (8-01)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 44.3333 Seconds
(without alignments)
33.062 Million cell updates/sec

Title: US-09-923-716C-1
Perfect score: 58
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	65.5	207	21	AAG29277	Arabidopsis thalia
2	38	65.5	262	18	AAW27262	Plant steroid 5-al
3	38	65.5	262	21	AAG29276	Arabidopsis thalia
4	38	65.5	394	23	ABB53569	Lactococcus lactis
5	37	63.8	560	22	ABG29423	Novel human diagno
6	36	62.1	82	22	AAO10186	Human polypeptide
7	35	60.3	242	21	AAG09307	Arabidopsis thalia
8	35	60.3	244	21	AAG07361	Arabidopsis thalia
9	35	60.3	244	21	AAG61263	Arabidopsis thalia
10	35	60.3	246	21	AAY32315	Soybean neutral tr
11	35	60.3	251	21	AAG07360	Arabidopsis thalia
12	35	60.3	251	21	AAG61262	Arabidopsis thalia
13	35	60.3	252	21	AAG09306	Arabidopsis thalia
14	35	60.3	254	21	AAG09305	Arabidopsis thalia
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16	35	60.3	254	23	ABB90980	Herbicidally activ
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19	34	58.6	56	21	AAG55171	Arabidopsis thalia
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21	34	58.6	57	21	AAG55170	Arabidopsis thalia
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25	34	58.6	264	22	AAM78329	Human protein SEQ
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32	34	58.6	322	22	AAG64294	Human GTP-binding
33	34	58.6	322	23	AAE21288	Human MrgX1 (mas-r
34	34	58.6	322	23	AAE17074	Human G-protein co
35	34	58.6	591	21	AAY58905	Rhinocladiella atr
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37	33.5	57.8	1810	22	ABB71194	Drosophila melanog
38	33	56.9	99	23	ABP41643	Human ovarian anti
39	33	56.9	310	21	AAB21021	Human nucleic acid
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42	33	56.9	609	20	AAW82727	Adenovirus Pig4KN
43	33	56.9	656	22	AAG90823	C glutamicum prote
44	33	56.9	700	22	AAB28610	Yeast RF1. Uniden
45	33	56.9	725	22	ABB68684	Drosophila melanog
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47	33	56.9	1235	23	ABB48680	Listeria monocytog
48	32	55.2	66	22	AAU55532	Propionibacterium
49	32	55.2	72	23	ABP33743	Human ORF2716 prot
50	32	55.2	74	23	AAO21674	Human secreted pro
51	32	55.2	93	22	AAM83247	Human immune/haema
52	32	55.2	137	22	AAU45923	Propionibacterium
53	32	55.2	156	22	AAU65539	Propionibacterium
54	32	55.2	283	23	ABB49253	Listeria monocytog
55	32	55.2	358	23	AAM52346	Hydratase-aldorase
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57	32	55.2	447	22	AAU03135	Streptococcus pyog
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59	32	55.2	447	23	ABP30002	Streptococcus poly
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62	32	55.2	462	21	AAY68843	Amino acid sequenc
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68	32	55.2	491	20	AAY41302	Tobacco anthranila
69	32	55.2	519	23	ABP27100	Streptococcus poly
70	32	55.2	526	23	ABB92684	Herbicidally activ
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73	32	55.2	577	20	AAW93815	Rice ASA first iso
74	32	55.2	577	20	AAW93810	Rice anthranilate
75	32	55.2	595	23	ABB93363	Herbicidally activ

ALIGNMENTS

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AC AAG29277;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 34806.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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RESULT 2
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AC AAW27262;
XX
DT 23-APR-1998 (first entry)
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DE Plant steroid 5-alpha reductase DET2.
XX
KW Plant steroid 5-alpha reductase; Arabidopsis; DET2; pest resistance;
KW brassinolide biosynthesis; growth.
XX
OS Arabidopsis sp.
XX
PN WO9739112-A1.
XX
PD 23-OCT-1997.
XX
PF 14-APR-1997; 97WO-US06115.
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PR 18-APR-1996; 96US-0634475.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Chory J, Li J;
XX
DR WPI; 1997-526449/48.
DR N-PSDB; AAT91260.
XX
PT New isolated plant steroid 5-alpha reductase gene, DET2 - used to
PT develop products for e.g. increasing plant yield and pest resistance
PT or for producing plants with reduced stature
XX
PS Claim 4; Page 45-46; 70pp; English.
XX
CC The present sequence represents a novel plant steroid 5-alpha reductase,
CC DET2. Methods have also been developed for producing plants with
CC increased yield, as compared to wild-type. The DET2 polypeptides have
CC 5AR activity and are involved in the brassinolide biosynthesis pathway.
CC The products and methods can be used to produce modified plants which
CC can exhibit increased plant growth, increased crop yield or increased
CC biomass. The plants can also have increased resistance to pests and
CC pesticides. Inhibitors of DET2 can be used to cause loss of function of
CC DET2 resulting in, e.g. male sterile plants or reduced stature (dwarf
CC plants).
XX
SQ Sequence 262 AA;

Query Match 65.5%; Score 38; DB 18; Length 262;
Best Local Similarity 45.5%; Pred. No. 12;
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AC AAG29276;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 34805.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Db         93 RTIIYPLRLFR 103
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RESULT 4
ABB53569
ID ABB53569 standard; Protein; 394 AA.
XX
AC ABB53569;
XX
DT 16-MAY-2002 (first entry)
XX
DE Lactococcus lactis protein ycgB.
XX
KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX
OS Lactococcus lactis IL1403.
XX
PN FR2807446-A1.
XX
PD 12-OCT-2001.
XX
PF 11-APR-2000; 2000FR-0004630.
XX
PR 11-APR-2000; 2000FR-0004630.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
XX
DR WPI; 2002-043418/06.
XX
PT New nucleotide sequence useful in the identification or Lactococcus
PT lactis and related species -
XX
PS Claim 6; SEQ ID No 271; 2504pp; French.
XX
CC The present invention is related to a Lactococcus lactis nucleotide
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The
CC nucleic acid sequence is useful in the detection and/or amplification of
CC nucleic acid sequence, particularly to identify Lactococcus lactis or
CC related species. The proteins of the invention are useful for the
CC biosynthesis or biodegradation of a composition of interest. The
CC invention helps research in lactic bacteria, particularly useful in the
CC production of yogurt and cheese.
CC Note: The sequence data for this patent is based on equivalent patent
CC WO200177334 (published 18-OCT-2001) which is available in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 394 AA;

Query Match 65.5%; Score 38; DB 23; Length 394;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 TVVYPTMMF 10
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Db         47 TLIYPTMRF 55
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RESULT 5
ABG29423
ID ABG29423 standard; Protein; 560 AA.
XX
AC ABG29423;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #29414.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS93610.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 59782; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating

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CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   560 AA;

  Query Match             63.8%;  Score 37;  DB 22;  Length 560;
  Best Local Similarity   77.8%;  Pred. No. 46;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |:| |||||
Db        214 TLVIPTMMF 222


RESULT 6
AAO10186
ID   AAO10186 standard; Protein; 82 AA.
XX
AC   AAO10186;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 24078.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200164835-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US04927.
XX
PR   28-FEB-2000; 2000US-0515126.
PR   18-MAY-2000; 2000US-0577409.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-514838/56.
DR   N-PSDB; AAI90117.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing
PT   diagnosing and treating e.g. leukaemia, inflammation and immune
PT   disorders -
XX
PS   Claim 20; SEQ ID NO 24078; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC   the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   82 AA;

  Query Match             62.1%;  Score 36;  DB 22;  Length 82;
  Best Local Similarity   85.7%;  Pred. No. 8.2;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 YPTMMFK 11
              ||||:||
Db          1 YPTMIFK 7


RESULT 7
AAG09307
ID   AAG09307 standard; Protein; 242 AA.
XX
AC   AAG09307;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 7187.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
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PR   23-APR-1999;   99US-0130510.
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PR   28-APR-1999;   99US-0131449.
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PR   27-MAY-1999;   99US-0136392.
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PR   01-JUN-1999;   99US-0137222.
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PR 18-JUN-1999; 99US-0139461.
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PR 18-JUN-1999; 99US-0139463.
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PR 18-JUN-1999; 99US-0139763.
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PR 01-JUL-1999; 99US-0141842.
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PR 02-JUL-1999; 99US-0142055.
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PR 20-JUL-1999; 99US-0144884.
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PR 30-AUG-1999; 99US-0151303.
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PR 24-SEP-1999; 99US-0155659.
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PR 04-OCT-1999; 99US-0157117.
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PR 26-OCT-1999; 99US-0161361.
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PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 242;
Best Local Similarity 60.0%; Pred. No. 45;

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Qy          1 RTVVYPTMMF 10
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Db        186 RQLVYPTKLF 195


RESULT 8
AAG07361
ID   AAG07361 standard; Protein; 244 AA.
XX
AC   AAG07361;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 4485.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
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PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
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DT 18-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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Query Match 60.3%; Score 35; DB 21; Length 244;
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Db        188 RQLVYPTKLF 197
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AC AAY32315;
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DT 28-FEB-2000 (first entry)

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XX
KW Triacylglycerol lipase; soybean; fatty acid; seed oil;
KW vegetable oil; transgenic plant.
XX
OS Glycine max.
XX
PN WO9955883-A2.
XX
PD 04-NOV-1999.
XX
PF 29-APR-1999; 99WO-US09280.
XX
PR 30-APR-1998; 98US-0083688.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon EB, Cahoon RE, Kinney AJ, Rafalski JA;
XX
DR WPI; 2000-062036/05.
DR N-PSDB; AAZ34964.
XX
PT Novel plant triacylglycerol lipase polynucleotides used to alter the
PT level of the enzyme in transgenic plants -
XX
PS Claim 10; Page 58-59; 65pp; English.
XX
CC This sequence represents most of a soybean neutral triacylglycerol
CC lipase (TAGL), as deduced from the nucleotide sequence of isolated
CC cDNA clones (see AAZ34964). Novel acid and neutral TAGL polypeptides
CC (see AAY32301-17) and polynucleotides (see AAZ34950-66) from corn,
CC Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes
CC may be prepared recombinantly and used to raise antibodies, which
CC are used for detecting the enzymes in situ in cells or in vitro in
CC cell extracts. The polynucleotides may be used to create transgenic
CC plants in which the TAGL levels are present at higher or lower levels
CC than normal, or in cell types or developmental processes where they are
CC not normally found. This would alter the level of triacylglycerol and
CC cholesteryl esters found in those cells. Accumulation of fatty acids
CC with unusual structures may be a positive phenotype in plants used for
CC foods. In addition, it may be desirable to eliminate expression of TAGL
CC genes for certain applications. TAGL enzymes may also be useful for the
CC processing of plant seed oils and for the development of novel seed
CC oils. The TAGL enzymes can also be used as targets to facilitate the
CC design and/or identification of inhibitors of those enzymes that may be
CC useful as herbicides. This is desirable because inhibition of the
CC activity of either of the enzymes could lead to an inhibition of plant
CC growth.
XX
SQ Sequence 246 AA;

Query Match 60.3%; Score 35; DB 21; Length 246;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db         75 ILYPTIMF 82
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 05-MAR-1999; 99US-0123180.
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PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 30-APR-1999; 99US-0132407.
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PR 06-MAY-1999; 99US-0132486.
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PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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Db        195 RQLVYPTKLF 204
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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XX
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XX
PD 06-SEP-2000.

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 252;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RTVVYPTMMF 10
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Db        196 RQLVYPTKLF 205
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RESULT 14
AAG09305
ID AAG09305 standard; Protein; 254 AA.
XX
AC AAG09305;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7185.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
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PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 254;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
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Db 198 RQLVYPTKLF 207

RESULT 15
AAB86353
ID AAB86353 standard; Protein; 254 AA.
XX
AC AAB86353;
XX
DT 20-SEP-2001 (first entry)
XX
DE A. thaliana allene oxide cyclase protein SEQ ID 10.
XX
KW Allene oxide cyclase; jasmonic acid; plant; AOC; jasmonate biosynthesis;
KW signalling molecule; gene expression; stress response; perfume synthesis;
KW wound-induced signal cascade; defensive response; transgenic plant;
KW protease inhibitor synthesis; phytoalexin synthesis; alkaloid synthesis;
KW pathogen resistance; herbicide resistance; ultra-violet protection;
KW secondary metabolite production; male sterility; flower development;
KW seed formation; germination.
XX
OS Arabidopsis thaliana.
XX
PN WO200157224-A2.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-EP01148.
XX
PR 02-FEB-2000; 2000DE-1004468.
XX
PA (PFLA-) INST PFLANZENBIOCHEMIE.
XX
PI Ziegler J, Stenzel I, Hause B, Wasternack C;
XX
DR WPI; 2001-483438/52.
DR N-PSDB; AAH21490.
XX
PT Nucleic acid encoding plant allene oxide cyclase, useful for producing
PT transgenic plants with altered jasmonic acid synthesis, e.g. increased
PT resistance to pathogens -
XX
PS Claim 1b; Page 55-56; 66pp; German.
XX
CC This invention describes novel nucleic acids (I), encoding proteins
CC (II) with the activity of the allene oxide cyclase (AOC) involved in
CC jasmonate biosynthesis. Jasmonic acid (JA) is a signalling molecule
CC involved in: (i) altered gene expression in plants in response to
CC stress; and (ii) developmental processes. It is also an intermediate in
CC the wound-induced signal cascade and induces many defensive responses in
CC plants, including synthesis of protease inhibitors, phytoalexins,
CC alkaloids and perfumes. (I) is used: (i) to produce transgenic plants,
CC cells etc. with altered AOC activity, specifically altered resistance to
CC pathogens and herbivores, optimal plant/useful insect/pest interaction;
CC increased biomass, altered carbohydrate and nitrogen metabolism;
CC increased production of secondary metabolites (especially alkaloids
CC and/or phytoalexins), optimal ultra-violet protection; altered male
CC sterility and/or altered development, especially flower development, seed
CC formation and/or germination; (ii) for selective production of 9S/13S
CC (cis(+))-12-oxophytodienoic acid (III), a precursor of jasmonic acid
CC (JA); (iii) for isolation of homologous sequences; and (iv) to express
CC AOC in prokaryotic or eukaryotic cells or (in antisense orientation) to
CC inhibit its expression. (I) Makes possible large scale production of high
CC purity JA. (I) is very specific for production of (III) (contrast
CC non-enzymatic methods which produce mixtures of isomers) which is a
CC precursor for the natural enantiomer of JA. This sequence represents the
CC Arabidopsis thaliana AOC described in the invention.
XX
SQ Sequence 254 AA;

Query Match 60.3%; Score 35; DB 22; Length 254;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
| :|||| :|
Db 198 RQLVYPTKLF 207

RESULT 16
ABB90980
ID ABB90980 standard; Protein; 254 AA.
XX
AC ABB90980;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 191.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP09892.
XX
PR 28-AUG-2001; 2001WO-EP09892.
XX
PA (FARB) BAYER AG.
XX
PI Tietjen K, Weidler M;
XX
DR WPI; 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
XX
PS Claim 5; SEQ ID NO 191; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising

```
CC   aligning and comparing nucleic acid or amino acid sequences from plant
CC   with nucleic acid or amino acid sequences from non-plant organisms using
CC   suitable search parameters, where plant sequences having an E-value
CC   greater by a factor of 3 than the E-value of most similar non-plant
CC   sequences are selected. The polypeptides or nucleic acids encoding them
CC   are useful for identifying modulators. The identified modulators are
CC   useful as herbicides.
XX
SQ   Sequence   254 AA;

 Query Match             60.3%;  Score 35;  DB 23;  Length 254;
  Best Local Similarity   60.0%;  Pred. No. 47;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        198 RQLVYPTKLF 207


RESULT 17
AAG07359
ID   AAG07359 standard; Protein; 258 AA.
XX
AC   AAG07359;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 4483.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
PR   21-APR-1999;   99US-0130449.
PR   23-APR-1999;   99US-0130510.
PR   23-APR-1999;   99US-0130891.
PR   28-APR-1999;   99US-0131449.
PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
PR   05-MAY-1999;   99US-0132485.
PR   06-MAY-1999;   99US-0132486.
PR   06-MAY-1999;   99US-0132487.
PR   07-MAY-1999;   99US-0132863.
PR   11-MAY-1999;   99US-0134256.
PR   14-MAY-1999;   99US-0134218.
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PR   21-MAY-1999;   99US-0135353.
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PR   27-MAY-1999;   99US-0136392.
PR   28-MAY-1999;   99US-0136782.
PR   01-JUN-1999;   99US-0137222.
PR   03-JUN-1999;   99US-0137528.
PR   04-JUN-1999;   99US-0137502.
PR   07-JUN-1999;   99US-0137724.
PR   08-JUN-1999;   99US-0138094.
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PR   18-JUN-1999;   99US-0139463.
PR   18-JUN-1999;   99US-0139750.
PR   18-JUN-1999;   99US-0139763.
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PR   20-JUL-1999;   99US-0144352.
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PR   22-JUL-1999;   99US-0145087.
PR   22-JUL-1999;   99US-0145089.
PR   22-JUL-1999;   99US-0145192.
PR   23-JUL-1999;   99US-0145145.
PR   23-JUL-1999;   99US-0145218.
PR   23-JUL-1999;   99US-0145224.
PR   26-JUL-1999;   99US-0145276.
PR   27-JUL-1999;   99US-0145913.
PR   27-JUL-1999;   99US-0145918.
PR   27-JUL-1999;   99US-0145919.
PR   28-JUL-1999;   99US-0145951.
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PR   02-AUG-1999;   99US-0146388.
PR   02-AUG-1999;   99US-0146389.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 28-OCT-1999; 99US-0161920.
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PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 258;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db        202 RQLVYPTKLF 211
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match 60.3%; Score 35; DB 21; Length 258;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db        202 RQLVYPTKLF 211


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DT   18-OCT-2000  (first entry)
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XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
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PF   25-FEB-2000; 2000EP-0301439.
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PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.
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PR 04-OCT-1999; 99US-0157117.
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Query Match 58.6%; Score 34; DB 21; Length 56;
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RESULT 20
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DT 18-OCT-2000 (first entry)
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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XX
PN EP1033405-A2.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 05-MAR-1999; 99US-0123180.
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KW   hybridisation assay; genetic mapping; gene expression control; promoter;
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Query Match 58.6%; Score 34; DB 21; Length 57;
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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Query Match 58.6%; Score 34; DB 21; Length 264;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db        106 VVYPAVMF 113
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match 58.6%; Score 34; DB 21; Length 264;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db        106 VVYPAVMF 113
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RESULT 25
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ID AAM78329 standard; Protein; 264 AA.
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AC AAM78329;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 991.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK51462.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3215-3216; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 264 AA;

Query Match 58.6%; Score 34; DB 22; Length 264;
Best Local Similarity 62.5%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          3 VVYPTMMF 10
              ::|| |||
Db         97 ILYPVMMF 104
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Search completed: July 16, 2003, 14:33:11
Job time : 49.3333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2003, 14:31:07 ; Search time 15 Seconds
(without alignments)
21.577 Million cell updates/sec

Title: US-09-923-716C-1
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	65.5	246	4	US-08-634-475-3	Sequence 3, Appli
2	38	65.5	246	4	US-09-709-791-3	Sequence 3, Appli
3	38	65.5	262	4	US-08-634-475-2	Sequence 2, Appli
4	38	65.5	262	4	US-09-709-791-2	Sequence 2, Appli
5	34	58.6	591	4	US-09-352-159-46	Sequence 46, Appl
6	34	58.6	598	4	US-09-352-159-42	Sequence 42, Appl
7	33	56.9	700	4	US-08-274-121B-5	Sequence 5, Appli
8	32	55.2	462	4	US-09-352-159-6	Sequence 6, Appli
9	32	55.2	462	4	US-09-352-159-8	Sequence 8, Appli
10	32	55.2	462	4	US-09-352-168-6	Sequence 6, Appli
11	32	55.2	462	4	US-09-352-168-8	Sequence 8, Appli
12	32	55.2	463	4	US-09-352-159-11	Sequence 11, Appl
13	32	55.2	463	4	US-09-352-168-11	Sequence 11, Appl
14	32	55.2	468	2	US-08-959-011-3	Sequence 3, Appli
15	32	55.2	487	4	US-09-352-159-21	Sequence 21, Appl
16	32	55.2	487	4	US-09-352-168-21	Sequence 21, Appl
17	32	55.2	491	2	US-09-001-826-23	Sequence 23, Appl
18	32	55.2	554	4	US-09-352-159-17	Sequence 17, Appl
19	32	55.2	554	4	US-09-352-168-17	Sequence 17, Appl
20	32	55.2	577	4	US-09-486-382B-2	Sequence 2, Appli
21	32	55.2	577	4	US-09-486-382B-13	Sequence 13, Appl
22	32	55.2	595	3	US-08-604-789B-3	Sequence 3, Appli
23	32	55.2	595	4	US-09-312-721A-3	Sequence 3, Appli
24	32	55.2	598	4	US-09-352-159-40	Sequence 40, Appl
25	32	55.2	600	4	US-09-352-159-23	Sequence 23, Appl
26	32	55.2	600	4	US-09-352-159-36	Sequence 36, Appl
27	32	55.2	600	4	US-09-352-159-38	Sequence 38, Appl
28	32	55.2	600	4	US-09-352-168-23	Sequence 23, Appl
29	32	55.2	692	4	US-09-352-159-19	Sequence 19, Appl
30	32	55.2	692	4	US-09-352-168-19	Sequence 19, Appl
31	32	55.2	829	4	US-09-352-159-33	Sequence 33, Appl
32	32	55.2	829	4	US-09-352-168-33	Sequence 33, Appl
33	32	55.2	991	4	US-09-352-159-27	Sequence 27, Appl
34	32	55.2	991	4	US-09-352-168-27	Sequence 27, Appl
35	32	55.2	1000	4	US-09-352-159-25	Sequence 25, Appl
36	32	55.2	1000	4	US-09-352-168-25	Sequence 25, Appl
37	32	55.2	1196	4	US-09-352-159-31	Sequence 31, Appl
38	32	55.2	1196	4	US-09-352-168-31	Sequence 31, Appl
39	32	55.2	1205	4	US-09-352-159-29	Sequence 29, Appl
40	32	55.2	1205	4	US-09-352-168-29	Sequence 29, Appl
41	31	53.4	125	2	US-08-408-095-35	Sequence 35, Appl
42	31	53.4	149	4	US-09-134-001C-2957	Sequence 2957, Ap
43	31	53.4	201	2	US-08-933-750C-21	Sequence 21, Appl
44	31	53.4	201	4	US-09-234-613-21	Sequence 21, Appl
45	31	53.4	320	2	US-08-933-750C-12	Sequence 12, Appl
46	31	53.4	320	4	US-09-234-613-12	Sequence 12, Appl
47	31	53.4	535	4	US-09-269-731-4	Sequence 4, Appli
48	31	53.4	1487	2	US-08-760-489-2	Sequence 2, Appli
49	31	53.4	1487	2	US-08-760-489-4	Sequence 4, Appli
50	31	53.4	1487	4	US-09-185-373-2	Sequence 2, Appli
51	31	53.4	1487	4	US-09-185-373-4	Sequence 4, Appli
52	31	53.4	3011	3	US-08-811-566-20	Sequence 20, Appl
53	31	53.4	3011	4	US-09-014-416-1	Sequence 1, Appli
54	31	53.4	3011	4	US-09-014-416-5	Sequence 5, Appli
55	31	53.4	3011	4	US-09-034-756-20	Sequence 20, Appl
56	31	53.4	3012	3	US-08-811-566-2	Sequence 2, Appli
57	31	53.4	3012	4	US-09-034-756-2	Sequence 2, Appli
58	30.5	52.6	371	4	US-09-574-141A-56	Sequence 56, Appl
59	30	51.7	280	6	5182210-12	Patent No. 5182210
60	30	51.7	451	1	US-08-625-322-4	Sequence 4, Appli
61	30	51.7	490	2	US-08-673-789-13	Sequence 13, Appl
62	30	51.7	621	3	US-08-604-789B-4	Sequence 4, Appli
63	30	51.7	621	4	US-09-312-721A-4	Sequence 4, Appli
64	30	51.7	697	2	US-08-674-351-4	Sequence 4, Appli
65	30	51.7	701	4	US-09-132-028-2	Sequence 2, Appli
66	30	51.7	722	4	US-09-134-001C-5482	Sequence 5482, Ap
67	30	51.7	744	1	US-08-162-809-20	Sequence 20, Appl
68	30	51.7	1437	3	US-09-061-400-2	Sequence 2, Appli
69	30	51.7	1453	2	US-09-001-273-2	Sequence 2, Appli
70	30	51.7	1453	4	US-08-843-459A-2	Sequence 2, Appli
71	29	50.0	17	4	US-09-227-357-426	Sequence 426, App
72	29	50.0	68	4	US-09-097-889-17	Sequence 17, Appl
73	29	50.0	156	4	US-09-134-001C-4450	Sequence 4450, Ap
74	29	50.0	305	4	US-08-858-207A-392	Sequence 392, App
75	29	50.0	401	4	US-09-134-001C-4403	Sequence 4403, Ap

ALIGNMENTS

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RESULT 1
US-08-634-475-3
; Sequence 3, Application US/08634475
; Patent No. 6143950
;  GENERAL INFORMATION:
;    APPLICANT:  Chory et al., Joanne
;    TITLE OF INVENTION:  NOVEL PLANT STEROID 5 alpha REDUCTASE,
;    TITLE OF INVENTION:  DET2
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/634,475
;      FILING DATE:  18-APR-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07251/015001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-634-475-3

  Query Match             65.5%;  Score 38;  DB 4;  Length 246;
  Best Local Similarity   45.5%;  Pred. No. 8.3;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         77 RTIIYPLRLFR 87


RESULT 2
US-09-709-791-3
; Sequence 3, Application US/09709791
; Patent No. 6352846
;   GENERAL INFORMATION:
;        APPLICANT: Chory, Joanne
;                   Li, Jianming
;        TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
;                            DET2
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
;             STREET: 620 Newport Center Drive, 16th floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/709,791
;             FILING DATE: 07-No. 6352846-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fuller, Michael
;             REGISTRATION NUMBER: 36,516
;             REFERENCE/DOCKET NUMBER: SALKINS.010DV1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/235-8550
;             TELEFAX: 619/235-0176
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 246 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: not relevant
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-709-791-3

  Query Match             65.5%;  Score 38;  DB 4;  Length 246;
  Best Local Similarity   45.5%;  Pred. No. 8.3;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         77 RTIIYPLRLFR 87


RESULT 3
US-08-634-475-2
; Sequence 2, Application US/08634475
; Patent No. 6143950
;  GENERAL INFORMATION:
;    APPLICANT:  Chory et al., Joanne
;    TITLE OF INVENTION:  NOVEL PLANT STEROID 5 alpha REDUCTASE,
;    TITLE OF INVENTION:  DET2
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/634,475
;      FILING DATE:  18-APR-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07251/015001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  262 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-634-475-2

  Query Match             65.5%;  Score 38;  DB 4;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 8.9;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 4
US-09-709-791-2
; Sequence 2, Application US/09709791
; Patent No. 6352846
;   GENERAL INFORMATION:
;        APPLICANT: Chory, Joanne
;                   Li, Jianming
;        TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
;                            DET2
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
;             STREET: 620 Newport Center Drive, 16th floor
;             CITY: Newport Beach
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;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/709,791
;             FILING DATE: 07-No. 6352846-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fuller, Michael
;             REGISTRATION NUMBER: 36,516
;             REFERENCE/DOCKET NUMBER: SALKINS.010DV1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/235-8550
;             TELEFAX: 619/235-0176
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 262 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: not relevant
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-709-791-2

  Query Match             65.5%;  Score 38;  DB 4;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 8.9;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||:::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 5
US-09-352-159-46
; Sequence 46, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 46
;   LENGTH: 591
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
US-09-352-159-46

  Query Match             58.6%;  Score 34;  DB 4;  Length 591;
  Best Local Similarity   55.6%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
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Db        405 TTLYPTLIF 413


RESULT 6
US-09-352-159-42
; Sequence 42, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 42
;   LENGTH: 598
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
US-09-352-159-42

  Query Match             58.6%;  Score 34;  DB 4;  Length 598;
  Best Local Similarity   55.6%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        406 TTLYPTLIF 414


RESULT 7
US-08-274-121B-5
; Sequence 5, Application US/08274121B
; Patent No. 6133034
;  GENERAL INFORMATION:
;    APPLICANT:  Arne Reidar Strom
;    APPLICANT:  Inga Kaasen
;    APPLICANT:  Olaf Bay Styrvold
;    APPLICANT:  John McDougall
;    TITLE OF INVENTION:  Methods and Compositions
;    TITLE OF INVENTION:  Related To The Production
;    TITLE OF INVENTION:  of Trehalose
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calgene, Inc.
;      STREET:  1920 Fifth Street
;      CITY:  Davis
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  95616
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 2.0 MB
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.1(a)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/274,121B
;      FILING DATE:  12-JULY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/893,099
;      FILING DATE:  27-MAY-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elizabeth Lassen
;      REGISTRATION NUMBER:  31,845
;      NAME:  Donna E. Scherer
;      REGISTRATION NUMBER:  34,719
;      REFERENCE/DOCKET NUMBER:  CGNE 86(1)
;    TELECOMMUNICATION INFORMATION:
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;      TELEPHONE:  (916) 753-6313
;      TELEFAX:  (916) 753-1510
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  700 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-274-121B-5

  Query Match             56.9%;  Score 33;  DB 4;  Length 700;
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  Matches    4;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              : ::|||  |
Db        672 KAIIYPTFFF 681


RESULT 8
US-09-352-159-6
; Sequence 6, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-6

  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 9
US-09-352-159-8
; Sequence 8, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-8

  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 10
US-09-352-168-6
; Sequence 6, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-168-6

  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 11
US-09-352-168-8
; Sequence 8, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-168-8
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  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 12
US-09-352-159-11
; Sequence 11, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-11

  Query Match             55.2%;  Score 32;  DB 4;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 13
US-09-352-168-11
; Sequence 11, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   OTHER INFORMATION: Extra lysine in the polypeptide sequence of
;   OTHER INFORMATION: K:trAPAO, 463 aa.
US-09-352-168-11

  Query Match             55.2%;  Score 32;  DB 4;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 14
US-08-959-011-3
; Sequence 3, Application US/08959011
; Patent No. 5932444
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  VACUOLAR ATPASE SUBUNIT AC45
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,011
;      FILING DATE:  Herewith
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0412 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  497984
US-08-959-011-3

  Query Match             55.2%;  Score 32;  DB 2;  Length 468;
  Best Local Similarity   87.5%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTM 8
              |||| |||
Db        244 RTVVPPTM 251


RESULT 15
US-09-352-159-21
; Sequence 21, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
```

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;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(24)
US-09-352-159-21

  Query Match             55.2%;  Score 32;  DB 4;  Length 487;
  Best Local Similarity   55.6%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        295 TTLYPTLTF 303


RESULT 16
US-09-352-168-21
; Sequence 21, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(24)
;   OTHER INFORMATION: K:trAPAO translational fusion with barley alpha
;   OTHER INFORMATION: amylase signal sequence, for expression and
;   OTHER INFORMATION: secretion of the mature trAPAO in maize.
US-09-352-168-21

  Query Match             55.2%;  Score 32;  DB 4;  Length 487;
  Best Local Similarity   55.6%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        295 TTLYPTLTF 303


RESULT 17
US-09-001-826-23
; Sequence 23, Application US/09001826A
; Patent No. 5965727
; GENERAL INFORMATION:
;  APPLICANT: SONG, HEE-SOOK
;  APPLICANT: BROTHERTON, JEFFREY E.
;  APPLICANT: WIDHOLM, JACK M.
;  TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
;  TITLE OF INVENTION: TRANSFORMATION
;  FILE REFERENCE: UI001.C1
;  CURRENT APPLICATION NUMBER: US/09/001,826A
;  CURRENT FILING DATE: 1997-12-31
;  EARLIER APPLICATION NUMBER: 08/937,739;  60/025,140
;  EARLIER FILING DATE: 1997-07-25; 1996-07-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: Macintosh Wordperfect converted to PC ASCII Text
; SEQ ID NO 23
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Nicotiana tabacum
US-09-001-826-23

  Query Match             55.2%;  Score 32;  DB 2;  Length 491;
  Best Local Similarity   71.4%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        422 RTIVFPT 428


RESULT 18
US-09-352-159-17
; Sequence 17, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 554
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(89)
US-09-352-159-17

  Query Match             55.2%;  Score 32;  DB 4;  Length 554;
  Best Local Similarity   55.6%;  Pred. No. 2.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        362 TTLYPTLTF 370


RESULT 19
US-09-352-168-17
; Sequence 17, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
```

```
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 554
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(89)
;   OTHER INFORMATION: yeast alpha mating factor secretion signal.
US-09-352-168-17

  Query Match             55.2%;  Score 32;  DB 4;  Length 554;
  Best Local Similarity   55.6%;  Pred. No. 2.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        362 TTLYPTLTF 370


RESULT 20
US-09-486-382B-2
; Sequence 2, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
;  APPLICANT: Hokko Chemical Industry Co., Ltd.
;  APPLICANT:  MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
;  TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
;  TITLE OF INVENTION:  synthase of rice, and DNAs related to said genes
;  FILE REFERENCE: 10647
;  CURRENT APPLICATION NUMBER: US/09/486,382B
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: JP 9-235049
;  PRIOR FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 577
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-09-486-382B-2

  Query Match             55.2%;  Score 32;  DB 4;  Length 577;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        508 RTIVFPT 514


RESULT 21
US-09-486-382B-13
; Sequence 13, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
;  APPLICANT: Hokko Chemical Industry Co., Ltd.
;  APPLICANT:  MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
;  TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
;  TITLE OF INVENTION:  synthase of rice, and DNAs related to said genes
;  FILE REFERENCE: 10647
;  CURRENT APPLICATION NUMBER: US/09/486,382B
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: JP 9-235049
;  PRIOR FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 577
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Modified amino acid sequence of Sequence No. 6388174 2
; Patent No. 6388174
US-09-486-382B-13

  Query Match             55.2%;  Score 32;  DB 4;  Length 577;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        508 RTIVFPT 514


RESULT 22
US-08-604-789B-3
; Sequence 3, Application US/08604789B
; Patent No. 6118047
;   GENERAL INFORMATION:
;        APPLICANT: Anderson, P.C.
;                   Chomet, P.S.
;                   Griffor, M.C.
;                   Kriz, A.L.
;        TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
;                            AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
;                            OVERPRODUCTION
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
;             STREET: P.O. Box 2938
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/604,789B
;             FILING DATE: 19-Jan-1996
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: <Unknown>
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Woessner, Warren D.
;             REGISTRATION NUMBER: 30,440
;             REFERENCE/DOCKET NUMBER: 950.026US1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (612) 373-6903
;             TELEFAX: (612) 339-3061
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 595 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-604-789B-3

  Query Match             55.2%;  Score 32;  DB 3;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 RTVVYPT 7
              ||:|:||
Db        526 RTIVFPT 532


RESULT 23
US-09-312-721A-3
; Sequence 3, Application US/09312721A
; Patent No. 6271016
;   GENERAL INFORMATION:
;        APPLICANT: Anderson, P.C.
;                   Chomet, P.S.
;                   Griffor, M.C.
;                   Kriz, A.L.
;        TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
;                            AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
;                            OVERPRODUCTION
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
;             STREET: P.O. Box 2938
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/312,721A
;             FILING DATE: 17-May-1999
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/604,789
;             FILING DATE: 19-JAN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Woessner, Warren D.
;             REGISTRATION NUMBER: 30,440
;             REFERENCE/DOCKET NUMBER: 950.026US2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (612) 373-6903
;             TELEFAX: (612) 339-3061
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 595 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-312-721A-3

  Query Match             55.2%;  Score 32;  DB 4;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        526 RTIVFPT 532


RESULT 24
US-09-352-159-40
; Sequence 40, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
;   LENGTH: 598
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (216)...(216)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-352-159-40

  Query Match             55.2%;  Score 32;  DB 4;  Length 598;
  Best Local Similarity   55.6%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        406 TTLYPTLTF 414


RESULT 25
US-09-352-159-23
; Sequence 23, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-23

  Query Match             55.2%;  Score 32;  DB 4;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        408 TTLYPTLTF 416


Search completed: July 16, 2003, 14:38:03
Job time : 22 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:33:19 ; Search time 27.6667 Seconds
(without alignments)
47.218 Million cell updates/sec

Title: US-09-923-716C-1
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	58.6	322	9	US-10-183-116-16	Sequence 16, Appl
2	34	58.6	322	9	US-10-079-384-4	Sequence 4, Appli
3	34	58.6	600	9	US-10-072-307-28	Sequence 28, Appl
4	34	58.6	600	9	US-10-072-307-30	Sequence 30, Appl
5	34	58.6	600	9	US-10-072-307-35	Sequence 35, Appl
6	34	58.6	600	9	US-10-072-307-37	Sequence 37, Appl
7	34	58.6	600	9	US-10-072-307-40	Sequence 40, Appl
8	34	58.6	600	9	US-10-072-307-43	Sequence 43, Appl
9	34	58.6	600	9	US-10-072-307-60	Sequence 60, Appl
10	34	58.6	600	9	US-10-072-307-64	Sequence 64, Appl
11	33	56.9	600	9	US-10-072-307-62	Sequence 62, Appl
12	33	56.9	656	9	US-09-738-626-4577	Sequence 4577, Ap
13	32	55.2	447	9	US-10-169-048-34	Sequence 34, Appl
14	32	55.2	447	9	US-10-169-048-44	Sequence 44, Appl
15	32	55.2	462	9	US-09-770-564-6	Sequence 6, Appli
16	32	55.2	462	9	US-09-770-564-8	Sequence 8, Appli
17	32	55.2	463	9	US-10-072-307-46	Sequence 46, Appl
18	32	55.2	463	9	US-10-072-307-47	Sequence 47, Appl
19	32	55.2	463	9	US-10-072-307-48	Sequence 48, Appl
20	32	55.2	463	9	US-10-072-307-50	Sequence 50, Appl
21	32	55.2	463	9	US-09-770-564-11	Sequence 11, Appl
22	32	55.2	487	9	US-09-770-564-21	Sequence 21, Appl
23	32	55.2	539	9	US-10-072-307-34	Sequence 34, Appl
24	32	55.2	554	9	US-09-770-564-17	Sequence 17, Appl
25	32	55.2	595	10	US-09-733-300-3	Sequence 3, Appli
26	32	55.2	600	9	US-10-072-307-26	Sequence 26, Appl
27	32	55.2	600	9	US-10-072-307-27	Sequence 27, Appl
28	32	55.2	600	9	US-10-072-307-29	Sequence 29, Appl
29	32	55.2	600	9	US-10-072-307-31	Sequence 31, Appl
30	32	55.2	600	9	US-10-072-307-32	Sequence 32, Appl
31	32	55.2	600	9	US-10-072-307-33	Sequence 33, Appl
32	32	55.2	600	9	US-10-072-307-36	Sequence 36, Appl
33	32	55.2	600	9	US-10-072-307-38	Sequence 38, Appl
34	32	55.2	600	9	US-10-072-307-41	Sequence 41, Appl
35	32	55.2	600	9	US-10-072-307-42	Sequence 42, Appl
36	32	55.2	600	9	US-10-072-307-44	Sequence 44, Appl
37	32	55.2	600	9	US-10-072-307-45	Sequence 45, Appl
38	32	55.2	600	9	US-10-072-307-52	Sequence 52, Appl
39	32	55.2	600	9	US-10-072-307-54	Sequence 54, Appl
40	32	55.2	600	9	US-10-072-307-56	Sequence 56, Appl
41	32	55.2	600	9	US-10-072-307-58	Sequence 58, Appl
42	32	55.2	600	9	US-10-072-307-66	Sequence 66, Appl
43	32	55.2	600	9	US-09-770-564-23	Sequence 23, Appl
44	32	55.2	692	9	US-09-770-564-19	Sequence 19, Appl
45	32	55.2	829	9	US-09-770-564-33	Sequence 33, Appl
46	32	55.2	991	9	US-09-770-564-27	Sequence 27, Appl
47	32	55.2	1000	9	US-09-770-564-25	Sequence 25, Appl
48	32	55.2	1196	9	US-09-770-564-31	Sequence 31, Appl
49	32	55.2	1205	9	US-09-770-564-29	Sequence 29, Appl
50	31	53.4	57	10	US-09-864-761-47860	Sequence 47860, A
51	31	53.4	58	9	US-09-764-891-2918	Sequence 2918, Ap
52	31	53.4	157	9	US-09-992-598-103	Sequence 103, App
53	31	53.4	157	9	US-09-989-293A-103	Sequence 103, App
54	31	53.4	157	9	US-09-989-735-103	Sequence 103, App
55	31	53.4	157	9	US-09-990-444-103	Sequence 103, App
56	31	53.4	157	9	US-09-989-730-103	Sequence 103, App
57	31	53.4	157	9	US-09-990-436-103	Sequence 103, App
58	31	53.4	157	9	US-09-991-181-103	Sequence 103, App
59	31	53.4	157	9	US-09-993-687-103	Sequence 103, App
60	31	53.4	157	9	US-09-989-734-103	Sequence 103, App
61	31	53.4	157	9	US-09-997-653-103	Sequence 103, App
62	31	53.4	157	9	US-10-174-590-90	Sequence 90, Appl
63	31	53.4	157	9	US-10-176-758-90	Sequence 90, Appl
64	31	53.4	157	9	US-10-175-737-90	Sequence 90, Appl
65	31	53.4	157	9	US-09-993-667-103	Sequence 103, App
66	31	53.4	157	9	US-10-173-706-90	Sequence 90, Appl
67	31	53.4	157	9	US-10-175-738-90	Sequence 90, Appl
68	31	53.4	157	9	US-10-175-752-90	Sequence 90, Appl
69	31	53.4	157	9	US-10-176-482-90	Sequence 90, Appl
70	31	53.4	157	9	US-10-176-757-90	Sequence 90, Appl
71	31	53.4	157	9	US-10-176-913-90	Sequence 90, Appl
72	31	53.4	157	9	US-10-180-552-90	Sequence 90, Appl
73	31	53.4	157	9	US-10-180-557-90	Sequence 90, Appl
74	31	53.4	157	9	US-09-990-438-103	Sequence 103, App
75	31	53.4	157	9	US-09-990-562-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-10-183-116-16
; Sequence 16, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CP1

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;  CURRENT APPLICATION NUMBER: US/10/183,116
;  CURRENT FILING DATE:  2002-06-26
;  PRIOR APPLICATION NUMBER: US 60/222,344
;  PRIOR FILING DATE: 2000-08-01
;  PRIOR APPLICATION NUMBER: US 60/202,027
;  PRIOR FILING DATE: 2000-05-04
;  PRIOR APPLICATION NUMBER: US 09/704,707
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: US 60/285,493
;  PRIOR FILING DATE: 2001-04-19
;  PRIOR APPLICATION NUMBER: US 09/849,869
;  PRIOR FILING DATE: 2001-05-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-183-116-16

  Query Match             58.6%;  Score 34;  DB 9;  Length 322;
  Best Local Similarity   62.5%;  Pred. No. 96;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              ::|| |||
Db         97 ILYPVMMF 104


RESULT 2
US-10-079-384-4
; Sequence 4, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
;  APPLICANT: Communi, Didier
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: 9409/2132
;  CURRENT APPLICATION NUMBER: US/10/079,384
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: US 09/885,453
;  PRIOR FILING DATE: 2001-06-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-079-384-4

  Query Match             58.6%;  Score 34;  DB 9;  Length 322;
  Best Local Similarity   62.5%;  Pred. No. 96;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              ::|| |||
Db         97 ILYPVMMF 104


RESULT 3
US-10-072-307-28
; Sequence 28, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 28
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_F7
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-28

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 4
US-10-072-307-30
; Sequence 30, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 30
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_G11
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-30

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 5
US-10-072-307-35
; Sequence 35, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
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;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 35
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F15C3
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-35

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 6
US-10-072-307-37
; Sequence 37, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 37
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F19F2
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-37

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 7
US-10-072-307-40
; Sequence 40, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 40
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F24F2
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-40

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 8
US-10-072-307-43
; Sequence 43, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 43
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F3B5
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-43

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 9
US-10-072-307-60
; Sequence 60, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 60
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;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 215
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 216
;   OTHER INFORMATION: Xaa = Gln, His
US-10-072-307-60

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 10
US-10-072-307-64
; Sequence 64, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 64
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 13
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 403
;   OTHER INFORMATION: Xaa = Val, Leu, Met
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 404
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 419
;   OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 433
;   OTHER INFORMATION: Xaa = Val, Leu, Met
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 443
;   OTHER INFORMATION: Xaa = Ter, Cys, Trp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 478
;   OTHER INFORMATION: Xaa = Leu, Ter, Ser, Trp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 489
;   OTHER INFORMATION: Xaa = Ter, Arg, Gly
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 538
;   OTHER INFORMATION: Xaa = Ter, Arg, Gly
US-10-072-307-64

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 11
US-10-072-307-62
; Sequence 62, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 62
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 187
;   OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 209
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 244
;   OTHER INFORMATION: Xaa = Glu, Asp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 262
;   OTHER INFORMATION: Xaa = Ter, Cys, Trp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 295
;   OTHER INFORMATION: Xaa = Tyr, Asn, Asp, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 299
;   OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 403
;   OTHER INFORMATION: Xaa = Val, Leu, Met
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 405
;   OTHER INFORMATION: Xaa = Ala, Thr, Pro, Ser
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 409
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```
;   OTHER INFORMATION: Xaa = Ala, Thr, Ser, Pro
US-10-072-307-62

  Query Match             56.9%;  Score 33;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 2.9e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TXLYPTLIF 416


RESULT 12
US-09-738-626-4577
; Sequence 4577, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/09/738,626
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4577
;   LENGTH: 656
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-4577

  Query Match             56.9%;  Score 33;  DB 9;  Length 656;
  Best Local Similarity   62.5%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              :: |||||
Db        307 IIMPTMMF 314


RESULT 13
US-10-169-048-34
; Sequence 34, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
;  APPLICANT: Clarke, Edna Elizabeth
;  APPLICANT:  Zhou, Liqing
;  APPLICANT:  Shea, Jacqueline Elizabeth
;  APPLICANT:  Feldman, Robert Graham
;  APPLICANT:  Holden, David William
;  TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their Use
;  FILE REFERENCE: GJE-97
;  CURRENT APPLICATION NUMBER: US/10/169,048
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: PCT/GB00/04997
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-10-169-048-34

  Query Match             55.2%;  Score 32;  DB 9;  Length 447;
  Best Local Similarity   45.5%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              :|::||   ||
Db        190 QTMIYPFTFFK 200


RESULT 14
US-10-169-048-44
; Sequence 44, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
;  APPLICANT: Clarke, Edna Elizabeth
;  APPLICANT:  Zhou, Liqing
;  APPLICANT:  Shea, Jacqueline Elizabeth
;  APPLICANT:  Feldman, Robert Graham
;  APPLICANT:  Holden, David William
;  TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their
;  FILE REFERENCE: GJE-97
;  CURRENT APPLICATION NUMBER: US/10/169,048
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: PCT/GB00/04997
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-10-169-048-44

  Query Match             55.2%;  Score 32;  DB 9;  Length 447;
  Best Local Similarity   45.5%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              :|::||   ||
Db        190 QTMIYPFTFFK 200


RESULT 15
US-09-770-564-6
; Sequence 6, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-770-564-6
```

```
  Query Match             55.2%;  Score 32;  DB 9;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 16
US-09-770-564-8
; Sequence 8, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-770-564-8

  Query Match             55.2%;  Score 32;  DB 9;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 17
US-10-072-307-46
; Sequence 46, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 46
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_TrH1
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-46

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 18
US-10-072-307-47
; Sequence 47, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 47
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_G6
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-47

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 19
US-10-072-307-48
; Sequence 48, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 48
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_H8
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-48

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
```

```
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 20
US-10-072-307-50
; Sequence 50, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 50
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_B6
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-50

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 21
US-09-770-564-11
; Sequence 11, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   OTHER INFORMATION: Extra lysine in the polypeptide sequence of
;   OTHER INFORMATION: K:trAPAO, 463 aa.
US-09-770-564-11

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 22
US-09-770-564-21
; Sequence 21, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(24)
;   OTHER INFORMATION: K:trAPAO translational fusion with barley alpha
;   OTHER INFORMATION: amylase signal sequence, for expression and
;   OTHER INFORMATION: secretion of the mature trAPAO in maize.
US-09-770-564-21

  Query Match             55.2%;  Score 32;  DB 9;  Length 487;
  Best Local Similarity   55.6%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        295 TTLYPTLTF 303


RESULT 23
US-10-072-307-34
; Sequence 34, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 34
;   LENGTH: 539
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F15A11
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-34

  Query Match             55.2%;  Score 32;  DB 9;  Length 539;
  Best Local Similarity   55.6%;  Pred. No. 3.9e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        347 TTLYPTLTF 355


RESULT 24
US-09-770-564-17
; Sequence 17, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 554
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(89)
;   OTHER INFORMATION: yeast alpha mating factor secretion signal.
US-09-770-564-17

  Query Match             55.2%;  Score 32;  DB 9;  Length 554;
  Best Local Similarity   55.6%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        362 TTLYPTLTF 370


RESULT 25
US-09-733-300-3
; Sequence 3, Application US/09733300
; Patent No. US20020061570A1
;   GENERAL INFORMATION:
;        APPLICANT: Anderson, P.C.
;                   Chomet, P.S.
;                   Griffor, M.C.
;                   Kriz, A.L.
;        TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
;                            AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
;                            OVERPRODUCTION
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
;             STREET: P.O. Box 2938
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/733,300
;             FILING DATE: 08-Dec-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/312,721
;             FILING DATE: 2000-09-11
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Woessner, Warren D.
;             REGISTRATION NUMBER: 30,440
;             REFERENCE/DOCKET NUMBER: 950.026US2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (612) 373-6903
;             TELEFAX: (612) 339-3061
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 595 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-733-300-3

  Query Match             55.2%;  Score 32;  DB 10;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 4.4e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        526 RTIVFPT 532


Search completed: July 16, 2003, 14:39:39
Job time : 39.6667 secs
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 20 Seconds
(without alignments)
52.874 Million cell updates/sec

Title: US-09-923-716C-1
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	70.7	333	2	S74406	hypothetical prote
2	41	70.7	974	2	T29545	hypothetical prote
3	38	65.5	262	2	C84800	3-oxo-5-alpha-ster
4	38	65.5	394	2	G86657	ABC transporter AT
5	37	63.8	395	2	H83424	hypothetical prote
6	35	60.3	180	2	D86267	T6J4.4 protein - A
7	35	60.3	435	2	E72342	pmbA-related prote
8	35	60.3	598	2	AG0890	probable arylsulfa
9	35	60.3	887	2	B96598	hypothetical prote
10	34	58.6	303	2	H84758	hypothetical prote
11	34	58.6	347	2	AD3513	channel protein vi
12	34	58.6	373	2	S17955	long-chain-fatty-a
13	34	58.6	373	2	S15161	long-chain-fatty-a
14	34	58.6	389	2	AD0478	acetylornithine de
15	34	58.6	404	2	B41317	O-antigen ligase c
16	34	58.6	404	2	AE0973	O-antigen ligase [
17	34	58.6	464	2	T50785	nucleoid DNA-bindi
18	34	58.6	674	2	D72329	hypothetical prote
19	34	58.6	711	2	A86424	unknown protein, 3
20	33.5	57.8	1724	2	T13942	UNC-13-B protein -
21	33	56.9	120	1	E69798	conserved hypothet
22	33	56.9	136	2	A90710	regulator of nucle
23	33	56.9	136	2	E85560	regulator of nucle
24	33	56.9	136	2	I57917	nucleoside diphosp
25	33	56.9	205	2	S29308	hypothetical prote
26	33	56.9	205	2	F83013	probable transcrip
27	33	56.9	221	2	AH0324	probable transport
28	33	56.9	261	2	T05447	hypothetical prote
29	33	56.9	390	2	AF3425	oxidoreductase (EC
30	33	56.9	394	2	S69870	hypothetical prote
31	33	56.9	531	2	D90453	hypothetical prote
32	33	56.9	551	2	D69282	glutamyl-tRNA synt
33	33	56.9	594	2	S00961	hypothetical prote
34	33	56.9	821	2	B75530	ATP-dependent prot
35	33	56.9	1021	2	T08601	hypothetical prote
36	33	56.9	1235	2	AC1358	ATP-dependent deox
37	33	56.9	1235	2	AC1728	ATP-dependent deox
38	32	55.2	61	1	F2RZKS	photosystem II pro
39	32	55.2	136	2	AC0578	regulator of nucle
40	32	55.2	142	2	G98072	7,8-dihydro-8-oxog
41	32	55.2	143	1	WMBE6H	transcription regu
42	32	55.2	143	2	T43976	transactivator [im
43	32	55.2	169	2	S72166	lipopolysaccharide
44	32	55.2	201	2	T07011	proteinase inhibit
45	32	55.2	203	2	E75413	conserved hypothet
46	32	55.2	214	2	G71318	hypothetical prote
47	32	55.2	214	2	D89985	hypothetical prote
48	32	55.2	214	2	T49174	hypothetical prote
49	32	55.2	283	2	T13879	maturase-like prot
50	32	55.2	283	2	AG1560	hypothetical prote
51	32	55.2	283	2	AI1202	hypothetical prote
52	32	55.2	285	2	T09308	immediate-early pr
53	32	55.2	334	2	T44163	hypothetical prote
54	32	55.2	421	2	S26246	glutamate/aspartat
55	32	55.2	458	2	A96938	polyA polymerase [
56	32	55.2	468	2	A55116	vacuolar ATPase (E
57	32	55.2	513	2	T40998	hypothetical prote
58	32	55.2	526	2	T49199	anthranilate synth
59	32	55.2	543	2	T22585	hypothetical prote
60	32	55.2	564	2	S15962	hypothetical prote
61	32	55.2	595	2	JQ1684	anthranilate synth
62	32	55.2	603	2	T11843	NADH2 dehydrogenas
63	32	55.2	620	2	T21391	hypothetical prote
64	32	55.2	1416	2	D71350	probable DNA-direc
65	32	55.2	1501	2	T29094	ribulose-bisphosph
66	32	55.2	1716	2	T14103	probable DNA-direc
67	32	55.2	3175	1	RRWVEV	genome polyprotein
68	31	53.4	80	2	A60450	hypothetical prote
69	31	53.4	95	2	B83814	Na+/H+ antiporter
70	31	53.4	104	2	T17649	hypothetical prote
71	31	53.4	105	2	T44098	hypothetical prote
72	31	53.4	142	2	G95207	MutT/nudix family
73	31	53.4	185	2	T29063	hypothetical prote
74	31	53.4	207	2	D65095	hypothetical prote
75	31	53.4	207	2	A98123	hypothetical prote

ALIGNMENTS

RESULT 1
S74406
hypothetical protein sll0456 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S74406
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74406
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-333 <KAN>
A;Cross-references: EMBL:D64001; GB:AB001339; NID:g1001102; PIDN:BAA10324.1; PID:d101
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 70.7%; Score 41; DB 2; Length 333;
Best Local Similarity 77.8%; Pred. No. 2.8;

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  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |||||||::|
Db        172 TVVYPTLVF 180


RESULT 2
T29545
hypothetical protein F48C1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29545
R;Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid F48C1.
A;Reference number: Z20638
A;Accession: T29545
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-974 <GAT>
A;Cross-references: EMBL:U97015; PIDN:AAB52345.1; GSPDB:GN00019; CESP:F48C1.1
A;Experimental source: strain Bristol N2; clone F48C1
C;Genetics:
A;Gene: CESP:F48C1.1
A;Map position: 1
A;Introns: 15/2; 58/3; 110/3; 150/1; 176/1; 267/2; 296/2; 326/2; 394/3; 441/1; 550/3; 59

  Query Match             70.7%;  Score 41;  DB 2;  Length 974;
  Best Local Similarity   60.0%;  Pred. No. 8.3;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :|::|| |||
Db        851 QTIIYPPMMF 860


RESULT 3
C84800
3-oxo-5-alpha-steroid 4-dehydrogenase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: C84800
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84800
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-262 <STO>
A;Cross-references: GB:AE002093; NID:g4895180; PIDN:AAD32767.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g38050
A;Map position: 2
C;Superfamily: Caenorhabditis elegans hypothetical protein ZK1251.3

  Query Match             65.5%;  Score 38;  DB 2;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 8.2;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 4
G86657
ABC transporter ATP binding protein ycgB [imported] - Lactococcus lactis subsp. lactis (
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: G86657
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86657
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <STO>
A;Cross-references: GB:AE005176; PID:g12723123; PIDN:AAK04361.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ycgB

  Query Match             65.5%;  Score 38;  DB 2;  Length 394;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |::|||| |
Db         47 TLIYPTMRF 55


RESULT 5
H83424
hypothetical protein PA1765 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83424
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <STO>
A;Cross-references: GB:AE004602; GB:AE004091; NID:g9947739; PIDN:AAG05154.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1765

  Query Match             63.8%;  Score 37;  DB 2;  Length 395;
  Best Local Similarity   60.0%;  Pred. No. 20;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | ||||:::|
Db        292 RQVVYPSLLF 301


RESULT 6
D86267
T6J4.4 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C;Accession: D86267
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86267
A;Status: preliminary
A;Molecule type: DNA
```

A;Residues: 1-180 <STO>
A;Cross-references: GB:AE005172; NID:g9958068; PIDN:AAG09557.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 180;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
| :|||| :|
Db 124 RQLVYPTKLF 133

RESULT 7
E72342
pmbA-related protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72342
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: E72342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-435 <ARN>
A;Cross-references: GB:AE001743; GB:AE000512; NID:g4981241; PIDN:AAD35809.1; PID:g498125
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0727
C;Superfamily: Escherichia coli pmbA protein

Query Match 60.3%; Score 35; DB 2; Length 435;
Best Local Similarity 54.5%; Pred. No. 53;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMFK 11
| |: ||:|:|
Db 135 RVVMVPTVMYK 145

RESULT 8
AG0890
probable arylsulfate sulfotransferase [imported] - Salmonella enterica subsp. enterica s
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AG0890
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AG0890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-598 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07717.1; PID:g16504269; GSPDB:GN00176
C;Genetics:
A;Gene: STY3370

Query Match 60.3%; Score 35; DB 2; Length 598;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVYPTMMFK 11
:|:|| |||
Db 590 LVHPTQMFK 598

RESULT 9
B96598
hypothetical protein T5A14.3 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96598
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-887 <STO>
A;Cross-references: GB:AE005173; NID:g4204259; PIDN:AAD10640.1; GSPDB:GN00141
C;Genetics:
A;Gene: T5A14.3
A;Map position: 1

Query Match 60.3%; Score 35; DB 2; Length 887;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TVVYPTMMFK 11
||| ||:| |
Db 696 TVVNPTLMLK 705

RESULT 10
H84758
hypothetical protein At2g34620 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84758
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84758
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <STO>
A;Cross-references: GB:AE002093; NID:g3128213; PIDN:AAC26693.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g34620
A;Map position: 2

Query Match 58.6%; Score 34; DB 2; Length 303;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
|| :|| ||
Db 120 RTELYPVFMF 129

RESULT 11
AD3513
channel protein virB6 homolog [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

```
C;Accession: AD3513
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AD3513
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53271.1; PID:g17984152; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0030
A;Map position: II

  Query Match             58.6%;  Score 34;  DB 2;  Length 347;
  Best Local Similarity   60.0%;  Pred. No. 65;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |:| | ||:|
Db        257 TIVMPYMMYK 266


RESULT 12
S17955
long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium lei
C;Species: Photobacterium leiognathi
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 03-Jun-2002
C;Accession: S17955
R;Lee, C.Y.; Szittner, R.B.; Meighen, E.A.
Eur. J. Biochem. 201, 161-167, 1991
A;Title: The lux genes of the luminous bacterial symbiont, Photobacterium leiognathi, of
coli.
A;Reference number: S17836; MUID:92007870; PMID:1915359
A;Accession: S17955
A;Molecule type: DNA
A;Residues: 1-373 <LEE>
A;Cross-references: EMBL:M63594; NID:g150687; PIDN:AAA25620.1; PID:g150692
C;Genetics:
A;Gene: luxE
C;Keywords: acid-thiol ligase
F;364/Active site: Cys (covalent substrate-binding) #status predicted

  Query Match             58.6%;  Score 34;  DB 2;  Length 373;
  Best Local Similarity   75.0%;  Pred. No. 70;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              |:|| |||
Db         78 VFPTSMFK 85


RESULT 13
S15161
long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium pho
N;Alternate names: acyl-protein synthetase
C;Species: Photobacterium phosphoreum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
C;Accession: S15161
R;Soly, R.R.; Meighen, E.A.
J. Mol. Biol. 219, 69-77, 1991
A;Title: Identification of the acyl transfer site of fatty acyl-protein synthetase from
A;Reference number: S15160; MUID:91218179; PMID:2023262
A;Accession: S15161
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-373 <JMO>
C;Genetics:
A;Gene: luxE
C;Keywords: acid-thiol ligase
F;364/Active site: Cys (covalent substrate-binding) #status predicted

  Query Match             58.6%;  Score 34;  DB 2;  Length 373;
  Best Local Similarity   75.0%;  Pred. No. 70;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              |:|| |||
Db         78 VFPTSMFK 85


RESULT 14
AD0478
acetylornithine deacetylase (EC 3.5.1.16) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
C;Accession: AD0478
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0478
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC93392.1; PID:g15981838; GSPDB:GN00175
C;Genetics:
A;Gene: argE
C;Superfamily: succinyl-diaminopimelate desuccinylase
C;Keywords: hydrolase

  Query Match             58.6%;  Score 34;  DB 2;  Length 389;
  Best Local Similarity   66.7%;  Pred. No. 73;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |: |||| |
Db        238 TIPYPTMNF 246


RESULT 15
B41317
O-antigen ligase complex protein rfaL - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 08-Oct-1999
C;Accession: B41317
R;MacLachlan, P.R.; Kadam, S.K.; Sanderson, K.E.
J. Bacteriol. 173, 7151-7163, 1991
A;Title: Cloning, characterization, and DNA sequence of the rfaLK region for lipopoly
A;Reference number: A41317; MUID:92041612; PMID:1657881
A;Accession: B41317
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <MAC>
A;Cross-references: GB:M73826; NID:g154328; PIDN:AAA27206.1; PID:g154330
C;Keywords: transmembrane protein

  Query Match             58.6%;  Score 34;  DB 2;  Length 404;
  Best Local Similarity   63.6%;  Pred. No. 76;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | |||  ||
Db        305 RVVDYPTWTFK 315


RESULT 16
AE0973
O-antigen ligase [imported] - Salmonella enterica subsp. enterica serovar Typhi (stra
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
```

```
C;Accession: AE0973
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AE0973
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03281.1; PID:g16504902; GSPDB:GN00176
C;Genetics:
A;Gene: waaL

  Query Match             58.6%;  Score 34;  DB 2;  Length 404;
  Best Local Similarity   63.6%;  Pred. No. 76;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | |||  ||
Db        305 RVVDYPTWTFK 315


RESULT 17
T50785
nucleoid DNA-binding protein cnd41-like protein - Arabidopsis thaliana
N;Alternate names: protein T30N20_30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50785
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25240
A;Accession: T50785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <BEV>
A;Cross-references: EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
C;Genetics:
A;Map position: 5
A;Introns: 58/1
A;Note: T30N20_30

  Query Match             58.6%;  Score 34;  DB 2;  Length 464;
  Best Local Similarity   66.7%;  Pred. No. 88;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              || |||: |
Db        392 TVTYPTIAF 400


RESULT 18
D72329
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72329
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72329
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-674 <ARN>
A;Cross-references: GB:AE001749; GB:AE000512; NID:g4981346; PIDN:AAD35899.1; PID:g498134
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0817

  Query Match             58.6%;  Score 34;  DB 2;  Length 674;
  Best Local Similarity   60.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :| |||  ||
Db        192 QTFVYPVFMF 201


RESULT 19
A86424
unknown protein, 35070-37205 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86424
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-711 <STO>
A;Cross-references: GB:AE005172; NID:g10092467; PIDN:AAG12869.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

  Query Match             58.6%;  Score 34;  DB 2;  Length 711;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |:|||: :
Db        461 RRVIYPTLRY 470


RESULT 20
T13942
UNC-13-B protein - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13942
R;Xu, X.Z.; Wes, P.D.; Chen, H.; Li, H.S.; Yu, M.; Morgan, S.; Liu, Y.; Montell, C.
J. Biol. Chem. 273, 31297, 1998
A;Title: Retinal targets for calmodulin include proteins implicated in synaptic trans
A;Reference number: Z17709; MUID:99030403; PMID:9813038
A;Accession: T13942
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1724 <XUX>
A;Cross-references: EMBL:Y17922; NID:g3893112; PIDN:CAA76942.1; PID:g3893113
C;Genetics:
A;Cross-references: FlyBase:FBgn0025726
A;Note: UNC-13-B
C;Superfamily: protein kinase C zinc-binding repeat homology
F;602-651/Domain: protein kinase C zinc-binding repeat homology <KZN>

  Query Match             57.8%;  Score 33.5;  DB 2;  Length 1724;
  Best Local Similarity   50.0%;  Pred. No. 4.2e+02;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    5;  Gaps    1;

Qy          1 RTVVYP-----TMMFK 11
              :|:| |     |||||
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Db       1437 KTIVLPPMTDKTMMFK 1452


RESULT 21
E69798
conserved hypothetical protein yetH - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: E69798
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69798
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-120 <KUN>
A;Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12535.1; PID:g2633029
A;Experimental source: strain 168
C;Genetics:
A;Gene: yetH
C;Superfamily: Bacillus probable methylglyoxalase yurT

  Query Match             56.9%;  Score 33;  DB 1;  Length 120;
  Best Local Similarity   54.5%;  Pred. No. 34;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | |:||  | |
Db         53 RLVIYPKAMMK 63


RESULT 22
A90710
regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157:H7
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: A90710
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A90710
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34072.1; PID:g13360107; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0649

  Query Match             56.9%;  Score 33;  DB 2;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 23
E85560
regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E85560
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85560
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <STO>
A;Cross-references: GB:AE005174; NID:g12513506; PIDN:AAG54945.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: rnk

  Query Match             56.9%;  Score 33;  DB 2;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 24
I57917
nucleoside diphosphate kinase regulator - Escherichia coli (strain K-12)
N;Alternate names: rnk protein
C;Species: Escherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 01-Mar-2002
C;Accession: I57917; H64794
R;Schlictman, D.; Shankar, S.; Chakrabarty, A.M.
Mol. Microbiol. 16, 309-320, 1995
A;Title: The Escherichia coli genes sspA and rnk can functionally replace the Pseudom
A;Reference number: I57917; MUID:96015444; PMID:7565093
A;Accession: I57917
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-136 <RES>
A;Cross-references: GB:L37900; NID:g598117; PIDN:AAC36933.1; PID:g598118
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64794
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-136 <BLAT>
A;Cross-references: GB:AE000166; GB:U00096; NID:g1786819; PIDN:AAC73711.1; PID:g17868
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: rnk

  Query Match             56.9%;  Score 33;  DB 2;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 25
S29308
hypothetical protein 3 (phaC2 3' region) - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999
```

C;Accession: S29308; S28380
R;Timm, A.; Steinbuechel, A.
Eur. J. Biochem. 209, 15-30, 1992
A;Title: Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid) gene locus c
A;Reference number: S29303; MUID:93011120; PMID:1396693
A;Accession: S29308
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <TIM>
A;Cross-references: EMBL:X66592; NID:g45388; PIDN:CAA47154.1; PID:g45394

Query Match 56.9%; Score 33; DB 2; Length 205;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 RTVVYPTMM 9
              ||||| ||
Db        172 RTVVYQIMM 180
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Search completed: July 16, 2003, 14:34:15
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 10.3333 Seconds
(without alignments)
44.152 Million cell updates/sec

Title: US-09-923-716C-1
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	65.5	262	1	DET2_ARATH	Q38944 arabidopsis
2	34	58.6	373	1	LUXE_PHOLE	P29334 photobacter
3	34	58.6	404	1	RFAL_SALTY	P26471 salmonella
4	33	56.9	136	1	RNK_ECOLI	P40679 escherichia
5	33	56.9	193	1	RCF1_DICDI	O96390 dictyosteli
6	33	56.9	551	1	SYE_ARCFU	O29979 archaeoglob
7	33	56.9	594	1	YKP3_KLULA	P05469 kluyveromyc
8	32	55.2	61	1	PSBK_ORYSA	P12162 oryza sativ
9	32	55.2	61	1	PSBK_WHEAT	P58273 triticum ae
10	32	55.2	143	1	B701_HSV6G	P30024 human herpe
11	32	55.2	169	1	COAD_CHRVI	P71154 chromatium
12	32	55.2	200	1	CAKB_COTJA	Q98855 coturnix co
13	32	55.2	201	1	IP23_LYCES	Q43502 lycopersico
14	32	55.2	214	1	Y473_TREPA	O83486 treponema p
15	32	55.2	421	1	GLTT_BACCA	P24944 bacillus ca
16	32	55.2	468	1	VAS1_BOVIN	P40682 bos taurus
17	32	55.2	595	1	TRPE_ARATH	P32068 arabidopsis
18	32	55.2	603	1	NU5M_HYLLA	P03919 hylobates l
19	32	55.2	1416	1	RPOC_TREPA	O83270 treponema p
20	32	55.2	1716	1	RPA1_RAT	O54889 rattus norv
21	32	55.2	3175	1	RPOA_EAV	P19811 equine arte
22	31	53.4	157	1	SMP1_HUMAN	O95807 homo sapien
23	31	53.4	207	1	YQJI_ECOLI	Q46872 escherichia
24	31	53.4	320	1	DNC_HUMAN	Q9hc21 homo sapien
25	31	53.4	362	1	MSP1_YEAST	P28737 saccharomyc
26	31	53.4	421	1	GLTT_BACST	P24943 bacillus st
27	31	53.4	437	1	SECY_BUCAI	P57571 buchnera ap
28	31	53.4	439	1	RHG1_HUMAN	Q07960 homo sapien
29	31	53.4	440	1	AK_CHLPN	Q9z610 chlamydia p
30	31	53.4	442	1	SECY_SYNY3	P77964 synechocyst
31	31	53.4	507	1	PDI_DATGL	Q9xf61 datisca glo
32	31	53.4	527	1	KITH_HSVSA	P21293 herpesvirus
33	31	53.4	601	1	NU5M_DASNO	O21335 dasypus nov
34	31	53.4	604	1	NU5M_HORSE	P48656 equus cabal
35	31	53.4	606	1	NU5M_BOVIN	P03920 bos taurus
36	31	53.4	606	1	NU5M_CERSI	O03205 ceratotheri
37	31	53.4	606	1	NU5M_EQUAS	P92485 equus asinu
38	31	53.4	606	1	NU5M_SHEEP	O78756 ovis aries
39	31	53.4	640	1	GIDA_ANASP	Q8yr87 anabaena sp
40	31	53.4	657	1	UVRB_CAMJE	Q9ppm7 campylobact
41	31	53.4	714	1	PBPF_BACSU	P38050 bacillus su
42	31	53.4	1067	1	EG52_XENLA	Q91783 xenopus lae
43	31	53.4	3358	1	PGCV_MOUSE	Q62059 mus musculu
44	31	53.4	4196	1	DYHC_SCHPO	O13290 schizosacch
45	30.5	52.6	1968	1	RRPO_PVMR	P17965 potato viru
46	30	51.7	61	1	PSBK_HORVU	P25877 hordeum vul
47	30	51.7	116	1	LUXE_PHOLU	P19842 photorhabdu
48	30	51.7	122	1	YJ41_YEAST	P47121 saccharomyc
49	30	51.7	149	1	YQBN_BACSU	P45930 bacillus su
50	30	51.7	158	1	IP2X_SOLTU	Q00782 solanum tub
51	30	51.7	193	1	RCF2_DICDI	Q9gps3 dictyosteli
52	30	51.7	221	1	KCY1_BORBU	O51154 borrelia bu
53	30	51.7	238	1	YG26_HAEIN	P44278 haemophilus
54	30	51.7	265	1	UL07_HSVSA	Q01028 herpesvirus
55	30	51.7	315	1	VC04_VACCV	P17370 vaccinia vi
56	30	51.7	316	1	VC04_VACCC	P21038 vaccinia vi
57	30	51.7	316	1	VC04_VARV	P34012 variola vir
58	30	51.7	352	1	GLN1_DAUCA	O22504 daucus caro
59	30	51.7	356	1	GLN1_MEDSA	P04078 medicago sa
60	30	51.7	356	1	GLN1_PHAVU	P04770 phaseolus v
61	30	51.7	356	1	GLNA_VIGAC	P32289 vigna aconi
62	30	51.7	358	1	GLNA_LACSA	P23712 lactuca sat
63	30	51.7	376	1	YG3W_YEAST	P53293 saccharomyc
64	30	51.7	378	1	LUXE_VIBHA	P14286 vibrio harv
65	30	51.7	416	1	PXN1_XENLA	P49263 xenopus lae
66	30	51.7	420	1	PUR2_LISIN	Q92ap4 listeria in
67	30	51.7	420	1	PUR2_LISMO	Q8y6c6 listeria mo
68	30	51.7	426	1	STE2_SACKL	P12384 saccharomyc
69	30	51.7	477	1	LYII_HUMAN	Q14108 homo sapien
70	30	51.7	477	1	LYII_RAT	P27615 rattus norv
71	30	51.7	497	1	YJ92_YEAST	P47158 saccharomyc
72	30	51.7	519	1	SNX2_HUMAN	O60749 homo sapien
73	30	51.7	519	1	SNX2_MOUSE	Q9cwk8 mus musculu
74	30	51.7	521	1	PEL1_SACPS	P79001 saccharomyc
75	30	51.7	536	1	CCA4_DROME	Q9ve00 drosophila

ALIGNMENTS

RESULT 1
DET2_ARATH
ID DET2_ARATH STANDARD; PRT; 262 AA.
AC Q38944; Q9SH83;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable steroid reductase DET2 (EC 1.3.99.-).
GN DET2 OR AT2G38050 OR T8P21.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=96185496; PubMed=8602526;
RA Li J., Nagpal P., Vitart V., McMorris T.C., Chory J.;
RT "A role for brassinosteroids in light-dependent development of
RT Arabidopsis.";
RL Science 272:398-401(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;

```
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RA   Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT   "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT   SSP consortium (Salk/Stanford/PGEC).";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Probably involved in a reduction step in the
CC       biosynthesis of the plant steroid, brassinolide. Defects in DET2
CC       leads to defects in light-regulated development.
CC   -!- PATHWAY: Brassinolide biosynthesis.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE STEROID 5-ALPHA REDUCTASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U53860; AAC49264.1; -.
DR   EMBL; AC007661; AAD32767.1; -.
DR   EMBL; AY045926; AAK76600.1; -.
DR   EMBL; AY079337; AAL85068.1; -.
DR   InterPro; IPR001104; Strd5A_dhC.
DR   Pfam; PF02544; Steroid_dh; 1.
DR   PROSITE; PS50244; S5A_REDUCTASE; 1.
KW   Oxidoreductase; Transmembrane.
FT   TRANSMEM     13     33       POTENTIAL.
FT   TRANSMEM     51     71       POTENTIAL.
FT   TRANSMEM    113    133       POTENTIAL.
FT   TRANSMEM    148    168       POTENTIAL.
FT   TRANSMEM    205    225       POTENTIAL.
FT   CONFLICT    198    198       C -> R (IN REF. 1).
SQ   SEQUENCE   262 AA;  30635 MW;  88291B8A8AF55664 CRC64;

  Query Match             65.5%;  Score 38;  DB 1;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 1.8;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 2
LUXE_PHOLE
ID   LUXE_PHOLE     STANDARD;      PRT;   373 AA.
AC   P29334;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE   protein synthetase).
GN   LUXE.
OS   Photobacterium leiognathi.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
OC   Photobacterium.
OX   NCBI_TaxID=658;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 25521;
RX   MEDLINE=92007870; PubMed=1915359;
RA   Lee C.Y., Szittner R.B., Meighen E.A.;
RT   "The lux genes of the luminous bacterial symbiont, Photobacterium
RT   leiognathi, of the ponyfish. Nucleotide sequence, difference in gene
RT   organization, and high expression in mutant Escherichia coli.";
RL   Eur. J. Biochem. 201:161-167(1991).
CC   -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC       IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC       FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC       SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC   -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC       an acyl-protein thiolester.
CC   -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M63594; AAA25620.1; -.
DR   PIR; S17955; S17955.
KW   Luminescence; Ligase.
SQ   SEQUENCE   373 AA;  43099 MW;  1B31848B00BF9921 CRC64;

  Query Match             58.6%;  Score 34;  DB 1;  Length 373;
  Best Local Similarity   75.0%;  Pred. No. 17;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              |:|| |||
Db         78 VFPTSMFK 85


RESULT 3
RFAL_SALTY
ID   RFAL_SALTY     STANDARD;      PRT;   404 AA.
AC   P26471;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   O-antigen ligase.
GN   RFAL OR WAAL OR RFBT OR STM3713.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RX   MEDLINE=92041612; PubMed=1657881;
RA   Maclachlan P.R., Kadam S.K., Sanderson K.E.;
RT   "Cloning, characterization, and DNA sequence of the rfaLK region for
RT   lipopolysaccharide synthesis in Salmonella typhimurium LT2.";
RL   J. Bacteriol. 173:7151-7163(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
CC   -!- FUNCTION: ADDS THE O-ANTIGEN ON THE GLUCOSE(II) GROUP OF LPS.
CC   -!- PATHWAY: Lipopolysaccharide core biosynthesis.
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CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: SHOWS ALMOST NO SIMILARITY TO E.COLI RFAL.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M73826; AAA27206.1; -.
DR   EMBL; AE008872; AAL22572.1; -.
DR   PIR; B41317; B41317.
DR   StyGene; SG10340; rfaL.
KW   Lipopolysaccharide biosynthesis; Ligase; Transmembrane;
KW   Complete proteome.
FT   TRANSMEM     66     84       POTENTIAL.
FT   TRANSMEM    184    203       POTENTIAL.
FT   TRANSMEM    227    244       POTENTIAL.
SQ   SEQUENCE   404 AA;  46034 MW;  1B84F7B3C757D2AB CRC64;

  Query Match             58.6%;  Score 34;  DB 1;  Length 404;
  Best Local Similarity   63.6%;  Pred. No. 19;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | |||  ||
Db        305 RVVDYPTWTFK 315


RESULT 4
RNK_ECOLI
ID   RNK_ECOLI      STANDARD;      PRT;   136 AA.
AC   P40679;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Regulator of nucleoside diphosphate kinase.
GN   RNK OR B0610 OR Z0754 OR ECS0649.
OS   Escherichia coli, and
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562, 83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96015444; PubMed=7565093;
RA   Schlictman D., Shankar S., Chakrabarty A.M.;
RT   "The Escherichia coli genes sspA and rnk can functionally replace the
RT   Pseudomonas aeruginosa alginate regulatory gene algR2.";
RL   Mol. Microbiol. 16:309-320(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA   Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA   Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97061202; PubMed=8905232;
RA   Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA   Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA   Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA   Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA   Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA   Yano M., Horiuchi T.;
RT   "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT   corresponding to the 12.7-28.0 min region on the linkage map.";
RL   DNA Res. 3:137-155(1996).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
CC   -!- FUNCTION: RNK AND SSPA CAN FUNCTIONALLY REPLACE P.AERUGINOSA
CC       ALGINATE REGULATORY GENE ALGR2.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L37900; AAC36933.1; -.
DR   EMBL; AE000166; AAC73711.1; -.
DR   EMBL; U82598; AAB40810.1; -.
DR   EMBL; D90701; BAA35239.1; -.
DR   EMBL; D90702; BAA35248.1; -.
DR   EMBL; AE005240; AAG54945.1; -.
DR   EMBL; AP002552; BAB34072.1; -.
DR   EcoGene; EG12637; rnk.
KW   Complete proteome.
SQ   SEQUENCE   136 AA;  14927 MW;  7043926623BA5E1E CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 9.8;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 5
RCF1_DICDI
ID   RCF1_DICDI     STANDARD;      PRT;   193 AA.
AC   O96390;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   RAS-related protein racF1.
GN   RACF1.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99214006; PubMed=10198067;
RA   Rivero F., Albrecht R., Dislich H., Bracco E., Graciotti L.,
RA   Bozzaro S., Noegel A.A.;
RT   "RacF1, a novel member of the Rho protein family in Dictyostelium
RT   discoideum, associates transiently with cell contact areas,
RT   macropinosomes and phagosomes.";
RL   Mol. Biol. Cell 10:1205-1219(1999).
CC   -!- FUNCTION: MIGHT ACT IN CONCERT AND/OR SHARE FUNCTIONS WITH OTHER
CC       MEMBERS OF THE RHO FAMILY IN THE REGULATION OF A SUBSET OF
CC       CYTOSKELETAL REARRANGEMENTS THAT ARE REQUIRED FOR THESE PROCESSES.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound.
CC   -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF037042; AAD09143.1; -.
DR   HSSP; P21181; 1AM4.
DR   DictyDb; DD?????; racF1.
DR   InterPro; IPR003578; GTPase_Rho.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR001806; Ras_trnsfrmng.
DR   InterPro; IPR005225; Small_GTP.
DR   Pfam; PF00071; ras; 1.
DR   PRINTS; PR00449; RASTRNSFRMNG.
DR   SMART; SM00174; RHO; 1.
DR   TIGRFAMs; TIGR00231; small_GTP; 1.
KW   GTP-binding; Prenylation; Lipoprotein.
FT   NP_BIND      10     17       GTP (BY SIMILARITY).
FT   NP_BIND      57     61       GTP (BY SIMILARITY).
FT   NP_BIND     115    118       GTP (BY SIMILARITY).
FT   DOMAIN       32     40       EFFECTOR REGION (POTENTIAL).
FT   LIPID       190    190       GERANYL-GERANYL (BY SIMILARITY).
SQ   SEQUENCE   193 AA;  21830 MW;  206E814C823E3B2E CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 193;
  Best Local Similarity   45.5%;  Pred. No. 14;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              |:|:||  : |
Db        173 RSVIYPNKLIK 183


RESULT 6
SYE_ARCFU
ID   SYE_ARCFU      STANDARD;      PRT;   551 AA.
AC   O29979;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE   (GluRS).
GN   GLTX OR AF0260.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC   Archaeoglobaceae; Archaeoglobus.
OX   NCBI_TaxID=2234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98049343; PubMed=9389475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulphate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC       diphosphate + L-glutamyl-tRNA(Glu).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AE001087; AAB90966.1; -.
DR   HSSP; P00962; 1GTR.
DR   TIGR; AF0260; -.
DR   InterPro; IPR004526; GltX_arch.
DR   InterPro; IPR000924; Glu_tRNA-synt_1c.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00749; tRNA-synt_1c; 1.
DR   PRINTS; PR00987; TRNASYNTHGLU.
DR   TIGRFAMs; TIGR00463; gltX_arch; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW   Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW   Complete proteome.
FT   SITE        100    110       "HIGH" REGION.
SQ   SEQUENCE   551 AA;  64402 MW;  A985A300C6B68F2E CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 551;
  Best Local Similarity   66.7%;  Pred. No. 41;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              |||||: |:
Db        270 VVYPTLDFE 278


RESULT 7
YKP3_KLULA
ID   YKP3_KLULA     STANDARD;      PRT;   594 AA.
AC   P05469;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Hypothetical killer plasmid PGKL-2 protein 3.
OS   Kluyveromyces lactis (Yeast).
OG   Plasmid pGKl-2.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX   NCBI_TaxID=28985;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140;
RX   MEDLINE=88289339; PubMed=3041369;
RA   Tommasino S., Ricci S., Galeotti C.L.;
RT   "Genome organization of the killer plasmid pGKL2 from Kluyveromyces
RT   lactis.";
RL   Nucleic Acids Res. 16:5863-5878(1988).
CC   -!- FUNCTION: THE PRESENCE OF THE TWO LINEAR PLASMIDS, TERMED
CC       PGKL1 AND PGKL2, IN STRAINS OF KLUYVEROMYCES LACTIS CONFERS
CC       THE KILLER PHENOTYPE TO THE HOST CELL, BY PROMOTING THE
CC       SECRETION OF A TOXIN ABLE TO INHIBIT THE GROWTH OF SENSITIVE
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CC       STRAINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X07776; CAA30604.1; -.
DR   PIR; S00961; S00961.
DR   InterPro; IPR000977; DNA_ligase.
DR   Pfam; PF01068; DNA_ligase; 1.
KW   Hypothetical protein; Plasmid.
SQ   SEQUENCE   594 AA;  70527 MW;  6AE57D37618BE6B0 CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 594;
  Best Local Similarity   36.4%;  Pred. No. 45;
  Matches    4;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              |: :|||:::|:
Db         80 RSTMYPSLIFR 90


RESULT 8
PSBK_ORYSA
ID   PSBK_ORYSA     STANDARD;      PRT;    61 AA.
AC   P12162;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Photosystem II reaction center protein K precursor (PSII-K).
GN   PSBK.
OS   Oryza sativa (Rice).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RX   MEDLINE=89364698; PubMed=2770692;
RA   Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA   Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA   Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura M.;
RT   "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT   intermolecular recombination between distinct tRNA genes accounts for
RT   a major plastid DNA inversion during the evolution of the cereals.";
RL   Mol. Gen. Genet. 217:185-194(1989).
CC   -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
CC       OF PHOTOSYSTEM II.
CC   -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X15901; CAA34010.1; -.
DR   PIR; JQ0203; F2RZKS.
DR   InterPro; IPR003687; PSII_PsbK.
DR   Pfam; PF02533; PsbK; 1.
KW   Photosystem II; Chloroplast.
FT   PROPEP          1     24       POTENTIAL.
FT   CHAIN          25     61       PHOTOSYSTEM II REACTION CENTER PROTEIN K.
SQ   SEQUENCE   61 AA;  6982 MW;  BBC361067C4158F5 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 61;
  Best Local Similarity   55.6%;  Pred. No. 6.9;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              :|:|||  |
Db         14 SVIYPTSFF 22


RESULT 9
PSBK_WHEAT
ID   PSBK_WHEAT     STANDARD;      PRT;    61 AA.
AC   P58273;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Photosystem II reaction center protein K precursor (PSII-K).
GN   PSBK.
OS   Triticum aestivum (Wheat).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Chinese Spring;
RA   Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shiina T.,
RA   Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
RA   Gojobori T., Murai R., Murai K., Matsuoka Y., Ohnishi Y., Tajiri H.,
RA   Tsunewaki K.;
RT   "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
RT   complete sequence and contig clones.";
RL   Plant Mol. Biol. Rep. 18:243-253(2000).
CC   -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
CC       OF PHOTOSYSTEM II.
CC   -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB042240; BAB47017.1; -.
DR   InterPro; IPR003687; PSII_PsbK.
DR   Pfam; PF02533; PsbK; 1.
KW   Photosystem II; Chloroplast.
FT   PROPEP          1     24       BY SIMILARITY.
FT   CHAIN          25     61       PHOTOSYSTEM II REACTION CENTER PROTEIN K.
SQ   SEQUENCE   61 AA;  7030 MW;  467901067C4158FD CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 61;
  Best Local Similarity   55.6%;  Pred. No. 6.9;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              :|:|||  |
Db         14 SVIYPTSFF 22


RESULT 10
B701_HSV6G
ID   B701_HSV6G.    STANDARD;      PRT;   143 AA.
AC   P30024;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Transcriptional regulatory protein B701.
OS   Human herpesvirus (type 6 / strain GS) (HHV6).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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OC   Betaherpesvirinae; Roseolovirus.
OX   NCBI_TaxID=10369;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92148942; PubMed=1310766;
RA   Geng Y., Chandran B., Josephs S.F., Wood C.;
RT   "Identification and characterization of a human herpesvirus 6 gene
RT   segment that trans activates the human immunodeficiency virus type 1
RT   promoter.";
RL   J. Virol. 66:1564-1570(1992).
CC   -!- FUNCTION: MAY BE RESPONSIBLE FOR MOST OF THE TRANS-ACTIVATING
CC       ACTIVITY ON THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROMOTER BY
CC       HHV-6. IT MAY FUNCTION BY DIRECTLY BINDING TO THE NF-KAPPAB
CC       SITE OR MAY INVOLVE CELLULAR FACTORS, SUCH AS NF-KAPPAB, EITHER
CC       DIRECTLY OR INDIRECTLY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M81789; -; NOT_ANNOTATED_CDS.
DR   PIR; A42186; WMBE6H.
KW   Transcription regulation; Trans-acting factor; Activator.
SQ   SEQUENCE   143 AA;  16385 MW;  D0CE4D7C2422AAD8 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 143;
  Best Local Similarity   50.0%;  Pred. No. 17;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :|::||  ||
Db         50 KTLLYPKTMF 59


RESULT 11
COAD_CHRVI
ID   COAD_CHRVI     STANDARD;      PRT;   169 AA.
AC   P71154;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Pantetheine-
DE   phosphate adenylyltransferase) (PPAT) (Dephospho-CoA
DE   pyrophosphorylase).
GN   COAD OR KDTB.
OS   Chromatium vinosum.
OC   Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
OC   Allochromatium.
OX   NCBI_TaxID=1049;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=D / ATCC 17899 / DSM 180;
RX   MEDLINE=96328257; PubMed=8765743;
RA   Moulis J.M.;
RT   "Molecular cloning and expression of the gene encoding Chromatium
RT   vinosum 2[4Fe-4S] ferredoxin.";
RL   Biochim. Biophys. Acta 1308:12-14(1996).
CC   -!- FUNCTION: REVERSIBLY TRANSFERS AN ADENYLYL GROUP FROM ATP TO 4'-
CC       PHOSPHOPANTETHEINE, YIELDING DEPHOSPHO-COA (DPCOA) AND
CC       PYROPHOSPHATE (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + pantetheine 4'-phosphate = diphosphate +
CC       dephospho-CoA.
CC   -!- PATHWAY: Coenzyme A (CoA) biosynthesis; fourth step.
CC   -!- SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE COAD FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U45327; AAC44332.1; -.
DR   HSSP; P23875; 1B6T.
DR   InterPro; IPR004821; Cyt_tran_rel.
DR   InterPro; IPR004820; Cytidylyltransf.
DR   InterPro; IPR001980; LPS_biosynth.
DR   Pfam; PF01467; Cytidylyltransf; 1.
DR   PRINTS; PR01020; LPSBIOSNTHSS.
DR   TIGRFAMs; TIGR00125; cyt_tran_rel; 1.
KW   Transferase; Nucleotidyltransferase; Coenzyme A biosynthesis.
SQ   SEQUENCE   169 AA;  18559 MW;  5126FD2BF32824AC CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 169;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYP 6
              ||||||
Db          2 RTVVYP 7


RESULT 12
CAKB_COTJA
ID   CAKB_COTJA     STANDARD;      PRT;   200 AA.
AC   Q98855;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Putative calcium-activated potassium channel beta subunit.
GN   CO6.
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97224079; PubMed=9070660;
RA   Oberst C., Weiskirchen R., Hartl M., Bister K.;
RT   "Suppression in transformed avian fibroblasts of a gene (CO6)
RT   encoding a membrane protein related to mammalian potassium channel
RT   regulatory subunits.";
RL   Oncogene 14:1109-1116(1997).
CC   -!- FUNCTION: POTASSIUM CHANNEL PROTEIN WHICH MAY MODULATE THE
CC       PROPERTIES OF THE PORE-FORMING ALPHA SUBUNIT (BY SIMILARITY).
CC   -!- SUBUNIT: THE CALCIUM-ACTIVATED POTASSIUM CHANNEL IS COMPOSED OF
CC       AT LEAST TWO SUBUNITS: A PORE-FORMING ALPHA SUBUNIT AND A
CC       REGULATORY BETA SUBUNIT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U67865; AAC26967.1; -.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Ionic channel; Transmembrane; Glycoprotein.
FT   TRANSMEM     20     40       POTENTIAL.
FT   TRANSMEM    167    187       POTENTIAL.
FT   CARBOHYD     89     89       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   200 AA;  22677 MW;  B7A612D8973F711F CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 200;
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  Best Local Similarity   55.6%;  Pred. No. 23;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |  ::||:||
Db        169 TFLWPTLMF 177


RESULT 13
IP23_LYCES
ID   IP23_LYCES     STANDARD;      PRT;   201 AA.
AC   Q43502;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Proteinase inhibitor type II CEVI57 precursor.
GN   CEVI57.
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4081;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Rutgers; TISSUE=Leaf;
RX   MEDLINE=96252900; PubMed=8672818;
RA   Gadea J., Mayda E., Conejero V., Vera P.;
RT   "Characterization of defense-related genes ectopically expressed in
RT   viroid-infected tomato plants.";
RL   Mol. Plant Microbe Interact. 9:409-415(1996).
CC   -!- INDUCTION: BY VIROID INFECTION.
CC   -!- SIMILARITY: BELONGS TO THE POTATO TYPE II PROTEINASE INHIBITOR
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X94946; CAA64416.1; -.
DR   HSSP; P01080; 4SGB.
DR   InterPro; IPR003465; Prot_inhib.
DR   Pfam; PF02428; Prot_inhib_II; 3.
KW   Serine protease inhibitor; Repeat; Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    201       PROTEINASE INHIBITOR TYPE II CEVI57.
FT   REPEAT       27     83       1.
FT   REPEAT       84    143       2.
FT   REPEAT      144    199       3.
FT   ACT_SITE     32     33       INTERACTION WITH TRYPSIN (PROBABLE).
FT   ACT_SITE    147    148       INTERACTION WITH TRYPSIN (PROBABLE).
SQ   SEQUENCE   201 AA;  21419 MW;  A3FCAB93773D8590 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 201;
  Best Local Similarity   57.1%;  Pred. No. 23;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              :|::|||
Db        106 KTIIYPT 112


RESULT 14
Y473_TREPA
ID   Y473_TREPA     STANDARD;      PRT;   214 AA.
AC   O83486;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein TP0473.
GN   TP0473.
OS   Treponema pallidum.
OC   Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX   NCBI_TaxID=160;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nichols;
RX   MEDLINE=98332770; PubMed=9665876;
RA   Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA   Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA   Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA   Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA   McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA   Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA   Venter J.C.;
RT   "Complete genome sequence of Treponema pallidum, the syphilis
RT   spirochete.";
RL   Science 281:375-388(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001224; AAC65467.1; -.
DR   TIGR; TP0473; -.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM      4     23       POTENTIAL.
FT   TRANSMEM     35     57       POTENTIAL.
FT   TRANSMEM     67     89       POTENTIAL.
FT   TRANSMEM     96    118       POTENTIAL.
FT   TRANSMEM    128    150       POTENTIAL.
FT   TRANSMEM    155    177       POTENTIAL.
FT   TRANSMEM    187    209       POTENTIAL.
SQ   SEQUENCE   214 AA;  24001 MW;  1497AA7E15DFAE92 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 214;
  Best Local Similarity   66.7%;  Pred. No. 25;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              |||||  :|:
Db        186 RTVVYTSML 194


RESULT 15
GLTT_BACCA
ID   GLTT_BACCA     STANDARD;      PRT;   421 AA.
AC   P24944;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier
DE   protein).
GN   GLTT.
OS   Bacillus caldotenax.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1395;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93062018; PubMed=1359385;
RA   Tolner B., Poolman B., Konings W.N.;
RT   "Characterization and functional expression in Escherichia coli of
RT   the sodium/proton/glutamate symport proteins of Bacillus
RT   stearothermophilus and Bacillus caldotenax.";
RL   Mol. Microbiol. 6:2845-2856(1992).
CC   -!- FUNCTION: THIS CARRIER PROTEIN IS PART OF THE NA(+)-DEPENDENT,
CC       BINDING-PROTEIN-INDEPENDENT GLUTAMATE-ASPARTATE TRANSPORT SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
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CC   -!- SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
CC       (SDF, TC 2.A.23).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M86509; AAA22493.1; -.
DR   PIR; S26246; S26246.
DR   InterPro; IPR001991; Na/diCO_symp.
DR   Pfam; PF00375; SDF; 1.
DR   PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; 1.
DR   PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; 1.
KW   Transport; Transmembrane; Symport.
FT   DOMAIN        1      3       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      4     24       POTENTIAL.
FT   DOMAIN       25     43       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     44     64       POTENTIAL.
FT   DOMAIN       65     77       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     78     98       POTENTIAL.
FT   DOMAIN       99    148       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    149    169       POTENTIAL.
FT   DOMAIN      170    198       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    199    219       POTENTIAL.
FT   DOMAIN      220    222       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    223    243       POTENTIAL.
FT   DOMAIN      244    244       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    245    265       POTENTIAL.
FT   DOMAIN      266    306       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    307    327       POTENTIAL.
FT   DOMAIN      328    330       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    331    351       POTENTIAL.
FT   TRANSMEM    352    372       POTENTIAL.
FT   DOMAIN      373    421       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   421 AA;  45345 MW;  10ABBE12EDD1E7E4 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 421;
  Best Local Similarity   75.0%;  Pred. No. 50;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              ||| ||:|
Db        226 VVYATMLF 233


RESULT 16
VAS1_BOVIN
ID   VAS1_BOVIN     STANDARD;      PRT;   468 AA.
AC   P40682;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Vacuolar ATP synthase subunit S1 precursor (EC 3.6.3.14) (V-ATPase S1
DE   subunit) (V-ATPase S1 accessory protein) (V-ATPase Ac45 subunit).
GN   ATP6IP1 OR ATP6S1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 378-388.
RC   TISSUE=Adrenal chromaffin;
RX   MEDLINE=95014142; PubMed=7929063;
RA   Supek F., Supekova L., Mandiyan S., Pan Y.-C.E., Nelson H., Nelson N.;
RT   "A novel accessory subunit for vacuolar H(+)-ATPase from chromaffin
RT   granules.";
RL   J. Biol. Chem. 269:24102-24106(1994).
CC   -!- FUNCTION: VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY
CC       OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
CC   -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC       H(+)(Out).
CC   -!- SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U10039; AAA50752.1; -.
KW   ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
KW   Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    468       VACUOLAR ATP SYNTHASE SUBUNIT S1.
FT   TRANSMEM    418    438       POTENTIAL.
FT   CARBOHYD    167    167       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    258    258       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    271    271       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    294    294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    355    355       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    404    404       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   468 AA;  51781 MW;  BF2C42D56ABB1B6D CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 468;
  Best Local Similarity   87.5%;  Pred. No. 56;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTM 8
              |||| |||
Db        244 RTVVPPTM 251


RESULT 17
TRPE_ARATH
ID   TRPE_ARATH     STANDARD;      PRT;   595 AA.
AC   P32068;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Anthranilate synthase component I-1, chloroplast precursor
DE   (EC 4.1.3.27).
GN   ASA1 OR AT5G05730 OR MJJ3.14.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93005721; PubMed=1392592;
RA   Niyogi K.K., Fink G.R.;
RT   "Two anthranilate synthase genes in Arabidopsis: defense-related
RT   regulation of the tryptophan pathway.";
RL   Plant Cell 4:721-733(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=97471969; PubMed=9330910;
RA   Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA   Miyajima N., Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT   features of the 1.6 Mb regions covered by twenty physically assigned
RT   P1 clones.";
RL   DNA Res. 4:215-230(1997).
CC   -!- CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate +
CC       pyruvate + L-glutamate.
```

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CC   -!- PATHWAY: Tryptophan biosynthesis; first step.
CC   -!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II.
CC   -!- SUBCELLULAR LOCATION: Chloroplast (Probable).
CC   -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC       USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC       GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M92353; AAA32738.1; -.
DR   EMBL; AB005237; BAB09667.1; -.
DR   PIR; S27751; S27751.
DR   HSSP; Q06128; 1QDL.
DR   InterPro; IPR005256; Anth_synthI.
DR   InterPro; IPR000350; Chorismate_bind.
DR   Pfam; PF00425; chorismate_bind; 1.
DR   PRINTS; PR00095; ANTSNTHASEI.
DR   ProDom; PD000779; Chorismate_bind; 1.
DR   TIGRFAMs; TIGR00564; trpE_most; 1.
KW   Tryptophan biosynthesis; Lyase; Chloroplast; Transit peptide;
KW   Multigene family.
FT   TRANSIT       1      ?       CHLOROPLAST (POTENTIAL).
FT   CHAIN         ?    595       ANTHRANILATE SYNTHASE COMPONENT I-1.
SQ   SEQUENCE   595 AA;  66311 MW;  674175416A2726F0 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 72;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:|| 
Db        526 RTIVFPT 532


RESULT 18
NU5M_HYLLA
ID   NU5M_HYLLA     STANDARD;      PRT;   603 AA.
AC   P03919;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
GN   MTND5 OR ND5 OR NADH5.
OS   Hylobates lar (Common gibbon).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9580;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ester;
RA   Arnason U., Gullberg A., Xu X.;
RT   "A complete mitochondrial DNA molecule of the white-handed gibbon,
RT   Hylobates lar, and comparison among individual mitochondrial genes of
RT   all hominoid genera.";
RL   Hereditas 124:185-189(1996).
RN   [2]
RP   SEQUENCE OF 1-79 FROM N.A.
RX   MEDLINE=82242101; PubMed=6284948;
RA   Brown W.M., Prager E.M., Wang A., Wilson A.C.;
RT   "Mitochondrial DNA sequences of primates: tempo and mode of
RT   evolution.";
RL   J. Mol. Evol. 18:225-239(1982).
CC   -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X99256; CAA67638.1; -.
DR   EMBL; V00659; CAA24025.1; -.
DR   PIR; A00449; A00449.
DR   InterPro; IPR003916; NADHub_oxred5.
DR   InterPro; IPR001750; Oxidored_q1.
DR   InterPro; IPR001516; Oxidored_q1_N.
DR   Pfam; PF00361; oxidored_q1; 1.
DR   Pfam; PF00662; oxidored_q1_N; 1.
DR   PRINTS; PR01434; NADHDHGNASE5.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ   SEQUENCE   603 AA;  67360 MW;  3BFF99C6EA7BCE70 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 603;
  Best Local Similarity   71.4%;  Pred. No. 73;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VYPTMMF 10
              ::|||||
Db         48 LFPTMMF 54


RESULT 19
RPOC_TREPA
ID   RPOC_TREPA     STANDARD;      PRT;  1416 AA.
AC   O83270;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE   beta' chain) (RNA polymerase beta' subunit).
GN   RPOC OR TP0242.
OS   Treponema pallidum.
OC   Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX   NCBI_TaxID=160;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nichols;
RX   MEDLINE=98332770; PubMed=9665876;
RA   Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA   Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA   Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA   Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA   McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA   Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA   Venter J.C.;
RT   "Complete genome sequence of Treponema pallidum, the syphilis
RT   spirochete.";
RL   Science 281:375-388(1998).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC       ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC       BETA' CHAIN.
CC   -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001205; AAC65230.1; -.
DR   HSSP; Q9KWU6; 1HQM.
DR   TIGR; TP0242; -.
DR   InterPro; IPR000722; RNA_pol_A.
DR   InterPro; IPR002879; RNA_pol_A2.
DR   Pfam; PF00623; RNA_pol_A; 1.
DR   Pfam; PF01854; RNA_pol_A2; 2.
KW   Transferase; DNA-directed RNA polymerase; Transcription;
KW   Complete proteome.
SQ   SEQUENCE   1416 AA;  159789 MW;  78D0EB6A1CAF7C9C CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 1416;
  Best Local Similarity   71.4%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|||:
Db        486 RTIVYPS 492


RESULT 20
RPA1_RAT
ID   RPA1_RAT       STANDARD;      PRT;  1716 AA.
AC   O54889;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DNA-directed RNA polymerase I largest subunit (EC 2.7.7.6) (RNA
DE   polymerase I 194 kDa subunit) (RPA194).
GN   POLR1A OR RPO1-4 OR RPA1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98086309; PubMed=9422795;
RA   Hannan R.D., Hempel W.M., Cavanaugh A., Arino T., Dimitrov S.I.,
RA   Moss T., Rothblum L.;
RT   "Affinity purification of mammalian RNA polymerase I. Identification
RT   of an associated kinase.";
RL   J. Biol. Chem. 273:1257-1267(1998).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES. RNA POLYMERASE I IS ESSENTIALLY USED TO TRANSCRIBE
CC       RIBOSOMAL DNA UNITS.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 14
CC       DIFFERENT POLYPEPTIDES. THIS SUBUNIT IS THE LARGEST COMPONENT OF
CC       RNA POLYMERASE I.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC       FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC       PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC       III FOR 5S AND TRNA GENES.
CC   -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF025425; AAB94601.1; -.
DR   InterPro; IPR000722; RNA_pol_A.
DR   InterPro; IPR002879; RNA_pol_A2.
DR   Pfam; PF00623; RNA_pol_A; 1.
DR   Pfam; PF01854; RNA_pol_A2; 2.
KW   Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
KW   Zinc-finger; Nuclear protein.
FT   ZN_FING      64     80       C2H2-TYPE (POTENTIAL).
SQ   SEQUENCE   1716 AA;  194191 MW;  E8EE15BC23E60941 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 1716;
  Best Local Similarity   50.0%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |: || |: |
Db        224 TITYPAMVHK 233


RESULT 21
RPOA_EAV
ID   RPOA_EAV       STANDARD;      PRT;  3175 AA.
AC   P19811; Q88625;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   POL polyprotein (ORF1A/1B) [Contains: RNA-directed RNA polymerase
DE   (EC 2.7.7.48); Helicase; Protease (EC 3.4.21.-)].
GN   POL.
OS   Equine arteritis virus (EAV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC   Arteriviridae; Arterivirus.
OX   NCBI_TaxID=11047;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bucyrus;
RX   MEDLINE=91237805; PubMed=1851863;
RA   den Boon J.A., Snijder E.J., Chirnside E.D., de Vries A.A.F.,
RA   Horzinek M.C., Spaan W.J.M.;
RT   "Equine arteritis virus is not a togavirus but belongs to the
RT   coronaviruslike superfamily.";
RL   J. Virol. 65:2910-2920(1991).
RN   [2]
RP   SEQUENCE OF 1-17 FROM N.A.
RC   STRAIN=Bucyrus;
RX   MEDLINE=90287699; PubMed=2162519;
RA   de Vries A.A.F., Chirnside E.D., Bredenbeek P.J., Gravestein L.A.,
RA   Horzinek M.C., Spaan W.J.M.;
RT   "All subgenomic mRNAs of equine arteritis virus contain a common
RT   leader sequence.";
RL   Nucleic Acids Res. 18:3241-3247(1990).
CC   -!- FUNCTION: RNA-DIRECTED RNA POLYMERASE & POSSIBLE HELICASE. A
CC       ROLE FOR NTP-BINDING PROTEINS IN RNA DUPLEX UNWINDING HAS BEEN
CC       SUGGESTED. ALSO CONTAINS A PROTEASE DOMAIN.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- MISCELLANEOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
CC       FOR 1727-ASN AND 1728-LEU.
CC   -!- SIMILARITY: WITH THE POLYMERASE PROTEIN OF OTHER CORONAVIRUSES AND
CC       OF TOROVIRUSES.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S32.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X53459; CAA37539.1; ALT_SEQ.
DR   EMBL; X53459; CAA37540.1; ALT_SEQ.
DR   EMBL; X52277; CAA36520.1; -.
DR   PIR; S10158; S10158.
DR   PIR; A39925; RRWVEV.
DR   MEROPS; C31.UNW; -.
DR   MEROPS; C32.001; -.
DR   MEROPS; C33.001; -.
DR   MEROPS; S32.001; -.
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DR   InterPro; IPR000606; Viral_helicase1.
DR   Pfam; PF01443; Viral_helicase1; 1.
KW   RNA-directed RNA polymerase; Transferase; Helicase; ATP-binding;
KW   Hydrolase; Serine protease; Zinc-finger.
FT   CHAIN         1   1727       ORF1A.
FT   CHAIN      1728   3175       ORF1B.
FT   DOMAIN     1080   1220       TRYPSIN-LIKE SERINE PROTEASE.
FT   DOMAIN     1218   1506       HELICASE.
FT   DOMAIN     2098   2306       POLYMERASE.
FT   ACT_SITE   1103   1103       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   1129   1129       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   1184   1184       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ZN_FING    2368   2414       BY SIMILARITY.
FT   NP_BIND    2528   2535       ATP (BY SIMILARITY).
SQ   SEQUENCE   3175 AA;  345275 MW;  ED5C8BA0E31DE695 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 3175;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 YPTMMF 10
              ||||:|
Db       1369 YPTMLF 1374


RESULT 22
SMP1_HUMAN
ID   SMP1_HUMAN     STANDARD;      PRT;   157 AA.
AC   O95807;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Small membrane protein 1.
GN   SMP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hu G.;
RT   "A new member of the 18 kDa small membrane protein family in human.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21154917; PubMed=11230166;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a catalog of human genes and proteins: sequencing and
RT   analysis of 500 novel complete protein coding human cDNAs.";
RL   Genome Res. 11:422-435(2001).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANT VAL-58.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA   Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: STRONG, TO C21ORF4.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF081282; AAD17754.1; -.
DR   EMBL; AL136627; CAB66562.1; -.
DR   EMBL; AF458851; AAL51108.1; -.
DR   MIM; 605348; -.
KW   Transmembrane; Polymorphism.
FT   TRANSMEM     26     46       POTENTIAL.
FT   TRANSMEM     58     78       POTENTIAL.
FT   TRANSMEM     95    115       POTENTIAL.
FT   TRANSMEM    126    146       POTENTIAL.
FT   VARIANT      58     58       A -> V.
FT                                /FTId=VAR_013121.
FT   VARIANT     141    141       F -> L.
FT                                /FTId=VAR_007851.
SQ   SEQUENCE   157 AA;  17400 MW;  8CDF83AA23EBB1FA CRC64;

  Query Match             53.4%;  Score 31;  DB 1;  Length 157;
  Best Local Similarity   83.3%;  Pred. No. 29;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 VVYPTM 8
              |:||||
Db         44 VIYPTM 49


RESULT 23
YQJI_ECOLI
ID   YQJI_ECOLI     STANDARD;      PRT;   207 AA.
AC   Q46872;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein yqjI.
GN   YQJI OR B3071.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U28379; AAA89150.1; -.
DR   EMBL; AE000389; AAC76106.1; -.
DR   EcoGene; EG12954; yqjI.
DR   InterPro; IPR005149; PadR.
DR   Pfam; PF03551; PadR; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   207 AA;  23401 MW;  DD3D108D83E087F7 CRC64;

  Query Match             53.4%;  Score 31;  DB 1;  Length 207;
  Best Local Similarity   62.5%;  Pred. No. 39;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              |:|||: |
Db         99 VIYPTLDF 106


RESULT 24
DNC_HUMAN
```

```
ID   DNC_HUMAN      STANDARD;      PRT;   320 AA.
AC   Q9HC21;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling
DE   protein 1).
GN   SLC25A19 OR DNC OR MUP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   PubMed=11226231;
RA   Dolce V., Fiermonte G., Runswick M.J., Palmieri F., Walker J.E.;
RT   "The human mitochondrial deoxynucleotide carrier and its role in the
RT   toxicity of nucleoside antivirals.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Renard S., Mondesert G., Besnard F.;
RT   "MUP 1, a mitochondrial uncoupling protein.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Responsible for the uptake of deoxynucleotides into the
CC       matrix of the mitochondria. Transports all four deoxy NDPs, and,
CC       less efficiently, the corresponding dNTPs. Does not transport
CC       dNMPs, NMPs, deoxynucleosides, nucleosides, purines, or
CC       pyrimidines. Supply deoxynucleotides to the mitochondrial matrix
CC       for conversion to triphosphates and incorporation into
CC       mitochondrial DNA.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC       inner membrane.
CC   -!- TISSUE SPECIFICITY: Expressed in all tissues examined except for
CC       placenta. Highest levels in colon, kidney, lung, testis, spleen,
CC       and brain.
CC   -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC   -!- DISEASE: Likely to be medically important by providing the means
CC       of uptake into mitochondria of nucleoside analogs, leading to the
CC       mitochondrial impairment that underlies the toxic side effects of
CC       such drugs in the treatment of viral illnesses, including AIDS,
CC       and in cancer therapy.
CC   -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ251857; CAC27560.1; -.
DR   EMBL; AJ301616; CAC37793.1; -.
DR   EMBL; AF182404; AAG16903.1; -.
DR   EMBL; BC001075; AAH01075.1; -.
DR   EMBL; BC005120; AAH05120.1; -.
DR   Genew; HGNC:14409; SLC25A19.
DR   MIM; 606521; -.
DR   InterPro; IPR002067; Mit_carrier.
DR   InterPro; IPR001993; Mitoch_carrier.
DR   Pfam; PF00153; mito_carr; 3.
DR   PRINTS; PR00926; MITOCARRIER.
DR   PROSITE; PS00215; MITOCH_CARRIER; 2.
KW   Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT   TRANSMEM     19     39       POTENTIAL.
FT   TRANSMEM     87    107       POTENTIAL.
FT   TRANSMEM    122    142       POTENTIAL.
FT   TRANSMEM    173    193       POTENTIAL.
FT   TRANSMEM    293    313       POTENTIAL.
SQ   SEQUENCE   320 AA;  35511 MW;  57CE0F01D538B1BE CRC64;

  Query Match             53.4%;  Score 31;  DB 1;  Length 320;
  Best Local Similarity   45.5%;  Pred. No. 61;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              :|: ||  :||
Db        231 KTLTYPLDLFK 241


RESULT 25
MSP1_YEAST
ID   MSP1_YEAST     STANDARD;      PRT;   362 AA.
AC   P28737;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   MSP1 protein (TAT-binding homolog 4).
GN   MSP1 OR YTA4 OR YGR028W.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SF747-19D;
RX   MEDLINE=94043260; PubMed=8226973;
RA   Nakai M., Endo T., Hase T., Matsubara H.;
RT   "Intramitochondrial protein sorting. Isolation and characterization
RT   of the yeast MSP1 gene which belongs to a novel family of putative
RT   ATPases.";
RL   J. Biol. Chem. 268:24262-24269(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RX   MEDLINE=95274317; PubMed=7754704;
RA   Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehnle S.,
RA   Schwarzlose C., Vetter I., Feldmann H.;
RT   "Identification of a set of yeast genes coding for a novel family of
RT   putative ATPases with high similarity to constituents of the 26S
RT   protease complex.";
RL   Yeast 10:1141-1155(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RX   MEDLINE=97435481; PubMed=9290212;
RA   Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
RT   "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
RT   chromosome VII.";
RL   Yeast 13:1077-1090(1997).
RN   [4]
RP   SEQUENCE OF 280-362 FROM N.A.
RC   STRAIN=SC167;
RX   MEDLINE=92204135; PubMed=1552903;
RA   Lisowsky T.;
RT   "Dual function of a new nuclear gene for oxidative phosphorylation
RT   and vegetative growth in yeast.";
RL   Mol. Gen. Genet. 232:58-64(1992).
CC.  -!- FUNCTION: INVOLVED IN INTRAMITOCHONDRIAL SORTING OF PROTEINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC       outer membrane.
CC   -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X68055; CAA48191.1; -.
DR   EMBL; X81069; CAA56956.1; -.
DR   EMBL; Z72813; CAA97015.1; -.
DR   EMBL; X60722; -; NOT_ANNOTATED_CDS.
DR   PIR; S20468; S20468.
DR   PIR; S37410; S37410.
DR   SGD; S0003260; MSP1.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003959; AAA_ATPase_centr.
DR   InterPro; IPR003960; AAA_sub.
DR   Pfam; PF00004; AAA; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00674; AAA; 1.
KW   ATP-binding; Mitochondrion; Outer membrane; Transmembrane.
FT   DOMAIN        1     12       INTERMEMBRANE (POTENTIAL).
FT   TRANSMEM     13     28       POTENTIAL.
FT   DOMAIN       29    362       CYTOPLASMIC (POTENTIAL).
FT   NP_BIND     133    140       ATP (POTENTIAL).
SQ   SEQUENCE   362 AA;  40343 MW;  1B3562A32F47F434 CRC64;

  Query Match             53.4%;  Score 31;  DB 1;  Length 362;
  Best Local Similarity   62.5%;  Pred. No. 69;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMM 9
              :|:|| ||
Db        106 SVIYPLMM 113


Search completed: July 16, 2003, 14:34:57
Job time : 16.3333 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:45 ; Search time 41.6667 Seconds
(without alignments)
54.396 Million cell updates/sec

Title: US-09-923-716C-1
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	70.7	333	16	Q55184	Q55184 synechocyst
2	41	70.7	974	5	O01574	O01574 caenorhabdi
3	38	65.5	394	16	Q9CIU3	Q9ciu3 lactococcus
4	37	63.8	390	10	Q8VWX1	Q8vwx1 perilla fru
5	37	63.8	391	10	Q9ZPP7	Q9zpp7 perilla fru
6	37	63.8	395	16	Q9I2X4	Q9i2x4 pseudomonas
7	36	62.1	512	10	Q9LUC5	Q9luc5 arabidopsis
8	35	60.3	180	10	Q9FX69	Q9fx69 arabidopsis
9	35	60.3	254	10	Q93ZC5	Q93zc5 arabidopsis
10	35	60.3	258	10	Q9LS01	Q9ls01 arabidopsis
11	35	60.3	264	16	Q8ZLZ1	Q8zlz1 salmonella
12	35	60.3	282	10	Q94JV3	Q94jv3 arabidopsis
13	35	60.3	320	11	Q8VGS2	Q8vgs2 mus musculu
14	35	60.3	435	16	Q9WZI6	Q9wzi6 thermotoga
15	35	60.3	504	12	Q9EME6	Q9eme6 amsacta moo
16	35	60.3	598	16	Q8Z3N6	Q8z3n6 salmonella
17	35	60.3	705	5	Q8SWA5	Q8swa5 encephalito
18	35	60.3	733	10	Q8S7E2	Q8s7e2 oryza sativ
19	35	60.3	735	10	Q9FJR9	Q9fjr9 arabidopsis
20	35	60.3	887	10	Q9ZVV2	Q9zvv2 arabidopsis
21	35	60.3	1030	3	Q9HFQ9	Q9hfq9 emericella
22	34	58.6	54	12	Q84121	Q84121 influenzavi
23	34	58.6	173	13	Q8UUZ6	Q8uuz6 brachydanio
24	34	58.6	180	16	Q98ID0	Q98id0 rhizobium l
25	34	58.6	212	16	Q8XNC4	Q8xnc4 clostridium
26	34	58.6	217	17	Q9HHU4	Q9hhu4 halobacteri
27	34	58.6	303	10	O64685	O64685 arabidopsis
28	34	58.6	316	10	Q9LSV4	Q9lsv4 arabidopsis
29	34	58.6	320	17	Q8U223	Q8u223 pyrococcus
30	34	58.6	322	4	Q96LB2	Q96lb2 homo sapien
31	34	58.6	322	4	Q8TDD9	Q8tdd9 homo sapien
32	34	58.6	322	4	Q8TDD8	Q8tdd8 homo sapien
33	34	58.6	347	2	Q9KIS7	Q9kis7 brucella ab
34	34	58.6	347	16	Q8YDZ2	Q8ydz2 brucella me
35	34	58.6	373	2	P95523	P95523 photobacter
36	34	58.6	373	2	Q52100	Q52100 photobacter
37	34	58.6	389	16	Q8ZA85	Q8za85 yersinia pe
38	34	58.6	404	16	Q8Z2F8	Q8z2f8 salmonella
39	34	58.6	464	10	Q9LEW3	Q9lew3 arabidopsis
40	34	58.6	530	17	Q973Z9	Q973z9 sulfolobus
41	34	58.6	674	16	Q9WZS4	Q9wzs4 thermotoga
42	34	58.6	711	10	Q9C8R8	Q9c8r8 arabidopsis
43	33.5	57.8	1304	5	O96959	O96959 drosophila
44	33.5	57.8	1508	5	Q8T049	Q8t049 drosophila
45	33.5	57.8	1724	5	O96960	O96960 drosophila
46	33.5	57.8	1752	5	Q9U4K9	Q9u4k9 drosophila
47	33.5	57.8	1810	5	Q9V483	Q9v483 drosophila
48	33	56.9	120	16	O31535	O31535 bacillus su
49	33	56.9	159	8	Q950X8	Q950x8 tetrahymena
50	33	56.9	205	2	Q51516	Q51516 pseudomonas
51	33	56.9	205	16	Q9HUC4	Q9huc4 pseudomonas
52	33	56.9	221	16	Q8ZDB7	Q8zdb7 yersinia pe
53	33	56.9	237	10	Q8RX02	Q8rx02 arabidopsis
54	33	56.9	261	10	Q9SUW6	Q9suw6 arabidopsis
55	33	56.9	299	4	Q9NXA8	Q9nxa8 homo sapien
56	33	56.9	310	4	Q9Y6E6	Q9y6e6 homo sapien
57	33	56.9	390	16	Q8YFX4	Q8yfx4 brucella me
58	33	56.9	457	17	Q9HLH0	Q9hlh0 thermoplasm
59	33	56.9	457	17	Q978Q5	Q978q5 thermoplasm
60	33	56.9	474	10	Q43541	Q43541 lilium long
61	33	56.9	531	17	Q97V62	Q97v62 sulfolobus
62	33	56.9	703	12	Q83467	Q83467 porcine ade
63	33	56.9	725	5	Q9VD08	Q9vd08 drosophila
64	33	56.9	821	16	Q9RXG4	Q9rxg4 deinococcus
65	33	56.9	842	17	Q970B4	Q970b4 sulfolobus
66	33	56.9	1021	5	O15733	O15733 dictyosteli
67	33	56.9	1063	4	Q8TDZ7	Q8tdz7 homo sapien
68	33	56.9	1235	16	Q929A9	Q929a9 listeria in
69	33	56.9	1235	16	Q8Y511	Q8y511 listeria mo
70	33	56.9	1824	5	Q9U0Y5	Q9u0y5 leishmania
71	32	55.2	61	10	Q8S6G8	Q8s6g8 oryza sativ
72	32	55.2	132	8	Q956K0	Q956k0 rhodotorula
73	32	55.2	136	16	Q8XFN0	Q8xfn0 salmonella
74	32	55.2	143	12	Q9WT48	Q9wt48 human herpe
75	32	55.2	143	12	Q9DYD9	Q9dyd9 human herpe

ALIGNMENTS

RESULT 1
Q55184
ID Q55184 PRELIMINARY; PRT; 333 AA.
AC Q55184;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein sll0456.
GN SLL0456.

```
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX   NCBI_TaxID=1148;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC 6803;
RA   Tabata S.;
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96127529; PubMed=8590279;
RA   Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA   Sugiura M., Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT   region from map positions 64% to 92% of the genome.";
RL   DNA Res. 2:153-166(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97061201; PubMed=8905231;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA   Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA   Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
DR   EMBL; D64001; BAA10324.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   333 AA;  37436 MW;  676E7399E4499ED6 CRC64;

  Query Match             70.7%;  Score 41;  DB 16;  Length 333;
  Best Local Similarity   77.8%;  Pred. No. 6.5;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              ||||||::|
Db        172 TVVYPTLVF 180


RESULT 2
O01574
ID   O01574      PRELIMINARY;      PRT;   974 AA.
AC   O01574;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 111.6 kDa protein.
GN   F48C1.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Gattung S., Le T.T.;
RT   "The sequence of C. elegans cosmid F48C1.";
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U97015; AAB52345.1; -.
DR   InterPro; IPR000602; Glyco_hydro_38.
DR   Pfam; PF01074; Glyco_hydro_38; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   974 AA;  111586 MW;  C825EFA33FB2F964 CRC64;

  Query Match             70.7%;  Score 41;  DB 5;  Length 974;
  Best Local Similarity   60.0%;  Pred. No. 18;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :|::|| |||
Db        851 QTIIYPPMMF 860


RESULT 3
Q9CIU3
ID   Q9CIU3      PRELIMINARY;      PRT;   394 AA.
AC   Q9CIU3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   ABC transporter ATP binding protein.
GN   YCGB OR LL0263.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC   Streptococcaceae; Lactococcus.
OX   NCBI_TaxID=1360;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
DR   EMBL; AE006263; AAK04361.1; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR001140; ABCtranprtrTM.
DR   InterPro; IPR003439; ABC_transportr.
DR   Pfam; PF00664; ABC_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transportr; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   394 AA;  43946 MW;  2822CBC28AEA4C36 CRC64;

  Query Match             65.5%;  Score 38;  DB 16;  Length 394;
  Best Local Similarity   66.7%;  Pred. No. 29;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |::|||| |
Db         47 TLIYPTMRF 55


RESULT 4
Q8VWX1
ID   Q8VWX1      PRELIMINARY;      PRT;   390 AA.
AC   Q8VWX1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Delta-15 desaturase.
GN   FAD3.
OS   Perilla frutescens.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
```

```
OX   NCBI_TaxID=48386;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. OKDONG; TISSUE=DEVELOPING SEED;
RA   Kim K.-H., Hwang S.-K., Hwang Y.-S.;
RT   "Cloning of Perilla delta-15 desaturase.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF213482; AAL36934.1; -.
DR   InterPro; IPR001225; FA_desaturase.
DR   Pfam; PF00487; FA_desaturase; 1.
DR   ProDom; PD001081; FA_desaturase; 2.
SQ   SEQUENCE   390 AA;  44857 MW;  6959C941D47A15AB CRC64;

  Query Match             63.8%;  Score 37;  DB 10;  Length 390;
  Best Local Similarity   70.0%;  Pred. No. 44;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |:| | ||||
Db        241 TIVGPNMMFK 250


RESULT 5
Q9ZPP7
ID   Q9ZPP7      PRELIMINARY;      PRT;   391 AA.
AC   Q9ZPP7;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Omega-3 fatty acid desaturase.
GN   FAD3.
OS   Perilla frutescens.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
OX   NCBI_TaxID=48386;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. SUWON-8;
RX   MEDLINE=99205707; PubMed=10189709;
RA   Chung C.-H., Kim J.-L., Lee Y.-C., Choi Y.-L.;
RT   "Cloning and characterization of a seed-specific omega-3 fatty acid
RT   desaturase cDNA from Perilla frutescens.";
RL   Plant Cell Physiol. 40:114-118(1999).
DR   EMBL; AF047039; AAD15744.1; -.
DR   InterPro; IPR001225; FA_desaturase.
DR   Pfam; PF00487; FA_desaturase; 1.
DR   ProDom; PD001081; FA_desaturase; 2.
SQ   SEQUENCE   391 AA;  44931 MW;  6637E81654C17CEC CRC64;

  Query Match             63.8%;  Score 37;  DB 10;  Length 391;
  Best Local Similarity   70.0%;  Pred. No. 45;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |:| | ||||
Db        242 TIVGPNMMFK 251


RESULT 6
Q9I2X4
ID   Q9I2X4      PRELIMINARY;      PRT;   395 AA.
AC   Q9I2X4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Hypothetical protein PA1765.
GN   PA1765.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
DR   EMBL; AE004602; AAG05154.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   395 AA;  44670 MW;  FC183A433B2529C8 CRC64;

  Query Match             63.8%;  Score 37;  DB 16;  Length 395;
  Best Local Similarity   60.0%;  Pred. No. 45;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | ||||:::|
Db        292 RQVVYPSLLF 301


RESULT 7
Q9LUC5
ID   Q9LUC5      PRELIMINARY;      PRT;   512 AA.
AC   Q9LUC5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Cytochrome P450 (Putative cytochrome P450 protein).
GN   MIE1.20.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RA   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=20277480; PubMed=10819329;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT   features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT   clones.";
RL   DNA Res. 7:131-135(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA   Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA   Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA   Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA   Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA   Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA   Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA   Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT   "Full Length cDNA of gene MIE1.20 (GI:9294391).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR   EMBL; AB023038; BAB02401.1; -.
DR   EMBL; AY050827; AAK92762.1; -.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00385; P450.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   512 AA;  58442 MW;  19DDEEAD9C9BAF0B CRC64;
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  Query Match             62.1%;  Score 36;  DB 10;  Length 512;
  Best Local Similarity   63.6%;  Pred. No. 90;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | ||  |||
Db         80 RVVPYPLQMFK 90


RESULT 8
Q9FX69
ID   Q9FX69      PRELIMINARY;      PRT;   180 AA.
AC   Q9FX69;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   T6J4.4 protein.
GN   T6J4.4.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA   Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
RA   Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA   Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
RA   Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC011810; AAG09557.1; -.
SQ   SEQUENCE   180 AA;  19794 MW;  5DA0943DB333F332 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 180;
  Best Local Similarity   60.0%;  Pred. No. 51;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        124 RQLVYPTKLF 133


RESULT 9
Q93ZC5
ID   Q93ZC5      PRELIMINARY;      PRT;   254 AA.
AC   Q93ZC5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   At1g13280/T6J4_23.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA   Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA   Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA   Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA   Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA   Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA   Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA   Ecker J.R.;
RT   "Arabidopsis cDNA clones.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY057636; AAL15267.1; -.
SQ   SEQUENCE   254 AA;  27809 MW;  4D82FA4889242353 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 254;
  Best Local Similarity   60.0%;  Pred. No. 72;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        198 RQLVYPTKLF 207


RESULT 10
Q9LS01
ID   Q9LS01      PRELIMINARY;      PRT;   258 AA.
AC   Q9LS01;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Genomic DNA, chromosome 3, TAC clone:K13N2.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RA   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=20277480; PubMed=10819329;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT   features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT   clones.";
RL   DNA Res. 7:131-135(2000).
DR   EMBL; AB028607; BAA95765.1; -.
SQ   SEQUENCE   258 AA;  28398 MW;  42AF942E0E9AAB87 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 258;
  Best Local Similarity   60.0%;  Pred. No. 73;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        202 RQLVYPTKLF 211


RESULT 11
Q8ZLZ1
ID   Q8ZLZ1      PRELIMINARY;      PRT;   264 AA.
AC   Q8ZLZ1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative arylsulfate sulfotransferase.
GN   STM3192.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
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RL   Nature 413:852-856(2001).
DR   EMBL; AE008846; AAL22066.1; -.
KW   Transferase; Hypothetical protein; Complete proteome.
SQ   SEQUENCE   264 AA;  29462 MW;  2B3F39791813620F CRC64;

  Query Match             60.3%;  Score 35;  DB 16;  Length 264;
  Best Local Similarity   66.7%;  Pred. No. 74;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              :|:|| |||
Db        256 LVHPTQMFK 264


RESULT 12
Q94JV3
ID   Q94JV3      PRELIMINARY;      PRT;   282 AA.
AC   Q94JV3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   AT5g46920/MQD22_6.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA   Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA   Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA   Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
RA   Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA   Davis R.W., Theologis A., Ecker J.R.;
RT   "Arabidopsis cDNA clones.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF372919; AAK49635.1; -.
DR   InterPro; IPR000442; Intron_maturse2.
DR   Pfam; PF01348; Intron_maturas2; 1.
SQ   SEQUENCE   282 AA;  32875 MW;  89B0C6FFA2ABF4B8 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 282;
  Best Local Similarity   60.0%;  Pred. No. 79;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |||||: :
Db          9 RRVVYPTLRY 18


RESULT 13
Q8VGS2
ID   Q8VGS2      PRELIMINARY;      PRT;   320 AA.
AC   Q8VGS2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Olfactory receptor MOR187-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073074; AAL60737.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   320 AA;  36768 MW;  1FF2EBF1413280F1 CRC64;

  Query Match             60.3%;  Score 35;  DB 11;  Length 320;
  Best Local Similarity   75.0%;  Pred. No. 89;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMM 9
              ||:|| ||
Db         82 TVIYPKMM 89


RESULT 14
Q9WZI6
ID   Q9WZI6      PRELIMINARY;      PRT;   435 AA.
AC   Q9WZI6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PMBA-related protein.
GN   TM0727.
OS   Thermotoga maritima.
OC   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX   NCBI_TaxID=2336;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MSB8 / DSM 3109;
RX   MEDLINE=99287316; PubMed=10360571;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA   Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
DR   EMBL; AE001743; AAD35809.1; -.
DR   TIGR; TM0727; -.
DR   InterPro; IPR002510; PmbA_TldD.
DR   Pfam; PF01523; PmbA_TldD; 1.
KW   Complete proteome.
SQ   SEQUENCE   435 AA;  48306 MW;  C8764A342A975819 CRC64;

  Query Match             60.3%;  Score 35;  DB 16;  Length 435;
  Best Local Similarity   54.5%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | |: ||:|:|
Db        135 RVVMVPTVMYK 145


RESULT 15
Q9EME6
ID   Q9EME6      PRELIMINARY;      PRT;   504 AA.
AC   Q9EME6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   AMV260.
GN   AMV260.
OS   Amsacta moorei entomopoxvirus (AmEPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC   Entomopoxvirus B.
OX   NCBI_TaxID=28321;
RN   [1]
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RP   SEQUENCE FROM N.A.
RX   MEDLINE=20396580; PubMed=10936094;
RA   Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
RA   Moyer R.W.;
RT   "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
RT   Analysis and Comparison with Other Poxviruses.";
RL   Virology 274:120-139(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
RA   Moyer R.W.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF250284; AAG02966.1; -.
SQ   SEQUENCE   504 AA;  61862 MW;  ACA9BFFA559FAA50 CRC64;

  Query Match             60.3%;  Score 35;  DB 12;  Length 504;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              ||::|:::|:
Db        459 TVIFPSLLFR 468


RESULT 16
Q8Z3N6
ID   Q8Z3N6      PRELIMINARY;      PRT;   598 AA.
AC   Q8Z3N6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Probable arylsulfate sulfotransferase.
GN   STY3370.
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
DR   EMBL; AL627278; CAD07717.1; -.
KW   Transferase; Complete proteome.
SQ   SEQUENCE   598 AA;  66586 MW;  B5434F028A5421F0 CRC64;

  Query Match             60.3%;  Score 35;  DB 16;  Length 598;
  Best Local Similarity   66.7%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              :|:|| |||
Db        590 LVHPTQMFK 598


RESULT 17
Q8SWA5
ID   Q8SWA5      PRELIMINARY;      PRT;   705 AA.
AC   Q8SWA5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein ECU02_1230.
GN   ECU02_1230.
OS   Encephalitozoon cuniculi.
OC   Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX   NCBI_TaxID=6035;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GB-M1;
RA   Genoscope;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GB-M1;
RX   MEDLINE=21576510; PubMed=11719806;
RA   Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA   Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
RA   Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA   Weissenbach J., Vivares C.P.;
RT   "Genome sequence and gene compaction of the eukaryote parasite
RT   Encephalitozoon cuniculi.";
RL   Nature 414:450-453(2001).
DR   EMBL; AL590442; CAD25152.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   705 AA;  79649 MW;  235B834A40258AEF CRC64;

  Query Match             60.3%;  Score 35;  DB 5;  Length 705;
  Best Local Similarity   62.5%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMM 9
              ||:|||::
Db        570 TVIYPTLL 577


RESULT 18
Q8S7E2
ID   Q8S7E2      PRELIMINARY;      PRT;   733 AA.
AC   Q8S7E2;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 82.3 kDa protein.
GN   OSJNBA0057L21.15.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA   Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA   Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
RA   VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA   Salzberg S.L., White O., Fraser C.M.;
RT   "Oryza sativa chromosome 10 BAC OSJNBa0057L21 genomic sequence.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC087599; AAL79699.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   733 AA;  82297 MW;  24C8521E18220D9D CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 733;
  Best Local Similarity   60.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |||||: :
Db  .     462 RRVVYPTLRY 471


RESULT 19
Q9FJR9
ID   Q9FJR9      PRELIMINARY;      PRT;   735 AA.
```

```
AC   Q9FJR9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Similarity to maturase-related protein.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=98403884; PubMed=9734815;
RA   Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA   Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT   Sequence features of the regions of 1,367,185 bp covered by 19
RT   physically assigned P1 and TAC clones.";
RL   DNA Res. 5:203-216(1998).
DR   EMBL; AB013394; BAB10231.1; -.
DR   InterPro; IPR000442; Intron_maturse2.
DR   InterPro; IPR000477; RVTse.
DR   Pfam; PF01348; Intron_maturas2; 1.
DR   Pfam; PF00078; rvt; 1.
KW   RNA-directed DNA polymerase.
SQ   SEQUENCE   735 AA;  85179 MW;  3C4A940CDA6E1590 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 735;
  Best Local Similarity   60.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |||||: :
Db        462 RRVVYPTLRY 471


RESULT 20
Q9ZVV2
ID   Q9ZVV2      PRELIMINARY;      PRT;   887 AA.
AC   Q9ZVV2;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   T5A14.3 protein.
GN   T5A14.3.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA   Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA   Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA   Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC005223; AAD10640.1; -.
DR   HSSP; P17119; 3KAR.
DR   InterPro; IPR001752; kinesin_motor.
DR   Pfam; PF00225; kinesin; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW   ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ   SEQUENCE   887 AA;  99904 MW;  748B215B02E2E9BC CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 887;
  Best Local Similarity   70.0%;  Pred. No. 2.4e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              ||| ||:| |
Db        696 TVVNPTLMLK 705


RESULT 21
Q9HFQ9
ID   Q9HFQ9      PRELIMINARY;      PRT;  1030 AA.
AC   Q9HFQ9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chitinase.
GN   CHIC.
OS   Emericella nidulans (Aspergillus nidulans).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=5072;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FGSC 4;
RA   Specht C.A., Benfield B.B., Garcia J.J.;
RT   "Identification of bacteria-like chitinases in fungi.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF314225; AAG34171.1; -.
DR   HSSP; P10968; 2CWG.
DR   InterPro; IPR001579; Chitinase_18/2.
DR   InterPro; IPR001002; Chitin_binding_1.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   Pfam; PF00187; Chitin_bind_1; 1.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   ProDom; PD000471; Glyco_hydro_18; 1.
DR   ProDom; PD000609; Chitin_binding_1; 1.
DR   SMART; SM00270; ChtBD1; 2.
DR   PROSITE; PS01095; CHITINASE_18; 1.
DR   PROSITE; PS00026; CHITIN_BINDING; 1.
KW   Chitin-binding.
SQ   SEQUENCE   1030 AA;  112748 MW;  8EE1E64192AF03E5 CRC64;

  Query Match             60.3%;  Score 35;  DB 3;  Length 1030;
  Best Local Similarity   66.7%;  Pred. No. 2.7e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              || |||: |
Db        951 TVTYPTLTF 959


RESULT 22
Q84121
ID   Q84121      PRELIMINARY;      PRT;    54 AA.
AC   Q84121;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Influenza A/Shearwater/Australia/75 (H5N3), neuraminidase (Seg 6), 5'
DE   end (Fragment).
OS   Influenzavirus A.
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenza A viruses.
OX   NCBI_TaxID=11320;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83017869; PubMed=6927853;
RA   Blok J., Air G.M.;
RT   "Sequence variation at the 3' end of the neuraminidase gene from 39
RT   influenza type A viruses.";
RL   Virology 121:211-229(1982).
DR   EMBL; K01014; AAA43416.1; -.
DR   InterPro; IPR001860; GH_34.
DR   Pfam; PF00064; neur; 1.
FT   NON_TER      54      54
SQ   SEQUENCE   54 AA;  5916 MW;  B0BD49BBF05D0153 CRC64;
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```
  Query Match             58.6%;  Score 34;  DB 12;  Length 54;
  Best Local Similarity   75.0%;  Pred. No. 25;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTM 8
              :||||||:
Db         43 QTVVYPTI 50


RESULT 23
Q8UUZ6
ID   Q8UUZ6      PRELIMINARY;      PRT;   173 AA.
AC   Q8UUZ6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Alpha A crystallin.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LENS;
RA   Runkle S., Hill J., Kantorow M., Horwitz J., Posner M.;
RT   "Cloning and characterization of zebrafish (Danio rerio) alpha A-
RT   crystallin.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY035778; AAK61363.1; -.
DR   InterPro; IPR001436; Crystallin_alpha.
DR   InterPro; IPR003090; Crystallin_N.
DR   InterPro; IPR002068; Hsp20.
DR   Pfam; PF00525; crystallin; 1.
DR   Pfam; PF00011; HSP20; 1.
DR   PRINTS; PR00299; ACRYSTALLIN.
DR   ProDom; PD001193; Crystallin_N; 1.
DR   PROSITE; PS01031; HSP20; 1.
SQ   SEQUENCE   173 AA;  19714 MW;  301D743DB91BBC13 CRC64;

  Query Match             58.6%;  Score 34;  DB 13;  Length 173;
  Best Local Similarity   60.0%;  Pred. No. 77;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              ||: ||| :|
Db         12 RTLGYPTRLF 21


RESULT 24
Q98ID0
ID   Q98ID0      PRELIMINARY;      PRT;   180 AA.
AC   Q98ID0;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein mll2459.
GN   MLL2459.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
DR   EMBL; AP002999; BAB49586.1; -.
DR   InterPro; IPR005149; PadR.
DR   Pfam; PF03551; PadR; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   180 AA;  19909 MW;  D94F736B2855CF60 CRC64;

  Query Match             58.6%;  Score 34;  DB 16;  Length 180;
  Best Local Similarity   75.0%;  Pred. No. 80;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              |||||: |
Db         49 VVYPTLTF 56


RESULT 25
Q8XNC4
ID   Q8XNC4      PRELIMINARY;      PRT;   212 AA.
AC   Q8XNC4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein CPE0414.
GN   CPE0414.
OS   Clostridium perfringens.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC   Clostridiales; Clostridiaceae; Clostridium.
OX   NCBI_TaxID=1502;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=13 / TYPE A;
RX   PubMed=11792842;
RA   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA   Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT   "Complete genome sequence of Clostridium perfringens, an anaerobic
RT   flesh-eater.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR   EMBL; AP003186; BAB80120.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   212 AA;  24363 MW;  DB7E1E2AC94BE697 CRC64;

  Query Match             58.6%;  Score 34;  DB 16;  Length 212;
  Best Local Similarity   62.5%;  Pred. No. 94;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              :|| |:||
Db        205 IYPNMIFK 212


Search completed: July 16, 2003, 14:37:07
Job time : 45 secs
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 44.3333 Seconds
(without alignments)
33.062 Million cell updates/sec

Title: US-09-923-716C-2
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	65.5	207	21	AAG29277	Arabidopsis thalia
2	38	65.5	262	18	AAW27262	Plant steroid 5-al
3	38	65.5	262	21	AAG29276	Arabidopsis thalia
4	38	65.5	394	23	ABB53569	Lactococcus lactis
5	37	63.8	560	22	ABG29423	Novel human diagno
6	36	62.1	82	22	AAO10186	Human polypeptide
7	35	60.3	242	21	AAG09307	Arabidopsis thalia
8	35	60.3	244	21	AAG07361	Arabidopsis thalia
9	35	60.3	244	21	AAG61263	Arabidopsis thalia
10	35	60.3	246	21	AAY32315	Soybean neutral tr
11	35	60.3	251	21	AAG07360	Arabidopsis thalia
12	35	60.3	251	21	AAG61262	Arabidopsis thalia
13	35	60.3	252	21	AAG09306	Arabidopsis thalia
14	35	60.3	254	21	AAG09305	Arabidopsis thalia
15	35	60.3	254	22	AAB86353	A. thaliana allene
16	35	60.3	254	23	ABB90980	Herbicidally activ
17	35	60.3	258	21	AAG07359	Arabidopsis thalia
18	35	60.3	258	21	AAG61261	Arabidopsis thalia
19	34	58.6	56	21	AAG55171	Arabidopsis thalia
20	34	58.6	56	21	AAG60760	Arabidopsis thalia
21	34	58.6	57	21	AAG55170	Arabidopsis thalia
22	34	58.6	57	21	AAG60759	Arabidopsis thalia
23	34	58.6	264	21	AAG05880	Arabidopsis thalia
24	34	58.6	264	21	AAG51213	Arabidopsis thalia
25	34	58.6	264	22	AAM78329	Human protein SEQ
26	34	58.6	266	21	AAG51212	Arabidopsis thalia
27	34	58.6	267	21	AAG05879	Arabidopsis thalia
28	34	58.6	322	20	AAY30161	Human dorsal root
29	34	58.6	322	20	AAY30162	Human dorsal root
30	34	58.6	322	22	AAE12794	Human G protein co
31	34	58.6	322	22	AAU04371	Human G-protein co
32	34	58.6	322	22	AAG64294	Human GTP-binding
33	34	58.6	322	23	AAE21288	Human MrgX1 (mas-r
34	34	58.6	322	23	AAE17074	Human G-protein co
35	34	58.6	591	21	AAY58905	Rhinocladiella atr
36	34	58.6	598	21	AAY58903	Rhinocladiella atr
37	33.5	57.8	1810	22	ABB71194	Drosophila melanog
38	33	56.9	99	23	ABP41643	Human ovarian anti
39	33	56.9	310	21	AAB21021	Human nucleic acid
40	33	56.9	593	22	AAU51414	Propionibacterium
41	33	56.9	609	20	AAW82726	Adenovirus pACTSsi
42	33	56.9	609	20	AAW82727	Adenovirus Pig4KN
43	33	56.9	656	22	AAG90823	C glutamicum prote
44	33	56.9	700	22	AAB28610	Yeast RF1. Uniden
45	33	56.9	725	22	ABB68684	Drosophila melanog
46	33	56.9	750	20	AAW82728	Adenovirus PNSPig4
47	33	56.9	1235	23	ABB48680	Listeria monocytog
48	32	55.2	66	22	AAU55532	Propionibacterium
49	32	55.2	72	23	ABP33743	Human ORF2716 prot
50	32	55.2	74	23	AAO21674	Human secreted pro
51	32	55.2	93	22	AAM83247	Human immune/haema
52	32	55.2	137	22	AAU45923	Propionibacterium
53	32	55.2	156	22	AAU65539	Propionibacterium
54	32	55.2	283	23	ABB49253	Listeria monocytog
55	32	55.2	358	23	AAM52346	Hydratase-aldorase
56	32	55.2	446	20	AAY42113	Corn anthranilate
57	32	55.2	447	22	AAU03135	Streptococcus pyog
58	32	55.2	447	22	AAU03140	Streptococcus pyog
59	32	55.2	447	23	ABP30002	Streptococcus poly
60	32	55.2	462	21	AAY58906	Amino polyol amine
61	32	55.2	462	21	AAY58907	Amino polyol amine
62	32	55.2	462	21	AAY68843	Amino acid sequenc
63	32	55.2	462	21	AAY68844	Amino acid sequenc
64	32	55.2	463	21	AAY58909	Amino polyol amine
65	32	55.2	463	21	AAY68845	Amino acid sequenc
66	32	55.2	487	21	AAY58912	Amino polyol amine
67	32	55.2	487	21	AAY68848	An aminopolyol ami
68	32	55.2	491	20	AAY41302	Tobacco anthranila
69	32	55.2	519	23	ABP27100	Streptococcus poly
70	32	55.2	526	23	ABB92684	Herbicidally activ
71	32	55.2	554	21	AAY58910	Amino polyol amine
72	32	55.2	554	21	AAY68846	An aminopolyol ami
73	32	55.2	577	20	AAW93815	Rice ASA first iso
74	32	55.2	577	20	AAW93810	Rice anthranilate
75	32	55.2	595	23	ABB93363	Herbicidally activ

ALIGNMENTS

RESULT 1
AAG29277
ID AAG29277 standard; Protein; 207 AA.

XX
AC AAG29277;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34806.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR 23-APR-1999; 99US-0130510.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.

PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.
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PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
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PR 08-OCT-1999; 99US-0158232.
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PR 13-OCT-1999; 99US-0159293.
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PR 21-OCT-1999; 99US-0160815.
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PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 65.5%; Score 38; DB 21; Length 207;
Best Local Similarity 45.5%; Pred. No. 9.2;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RTVVYPTMMFK 11
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Db         38 RTIIYPLRLFR 48
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RESULT 2
AAW27262
ID AAW27262 standard; Protein; 262 AA.
XX
AC AAW27262;
XX
DT 23-APR-1998 (first entry)
XX
DE Plant steroid 5-alpha reductase DET2.
XX
KW Plant steroid 5-alpha reductase; Arabidopsis; DET2; pest resistance;
KW brassinolide biosynthesis; growth.
XX
OS Arabidopsis sp.
XX
PN WO9739112-A1.
XX
PD 23-OCT-1997.
XX
PF 14-APR-1997; 97WO-US06115.
XX
PR 18-APR-1996; 96US-0634475.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Chory J, Li J;
XX
DR WPI; 1997-526449/48.
DR N-PSDB; AAT91260.
XX
PT New isolated plant steroid 5-alpha reductase gene, DET2 - used to
PT develop products for e.g. increasing plant yield and pest resistance
PT or for producing plants with reduced stature
XX
PS Claim 4; Page 45-46; 70pp; English.
XX
CC The present sequence represents a novel plant steroid 5-alpha reductase,
CC DET2. Methods have also been developed for producing plants with
CC increased yield, as compared to wild-type. The DET2 polypeptides have
CC 5AR activity and are involved in the brassinolide biosynthesis pathway.
CC The products and methods can be used to produce modified plants which
CC can exhibit increased plant growth, increased crop yield or increased
CC biomass. The plants can also have increased resistance to pests and
CC pesticides. Inhibitors of DET2 can be used to cause loss of function of
CC DET2 resulting in, e.g. male sterile plants or reduced stature (dwarf
CC plants).
XX
SQ Sequence 262 AA;

Query Match 65.5%; Score 38; DB 18; Length 262;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103
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RESULT 3
AAG29276
ID AAG29276 standard; Protein; 262 AA.
XX
AC AAG29276;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34805.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
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PR   08-OCT-1999;   99US-0158232.
PR   12-OCT-1999;   99US-0158369.
PR   13-OCT-1999;   99US-0159293.
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PR   14-OCT-1999;   99US-0159329.
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PR   21-OCT-1999;   99US-0160815.
PR   22-OCT-1999;   99US-0160980.
PR   22-OCT-1999;   99US-0160981.
PR   22-OCT-1999;   99US-0160989.
PR   25-OCT-1999;   99US-0161404.
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PR   25-OCT-1999;   99US-0161406.
PR   26-OCT-1999;   99US-0161359.
PR   26-OCT-1999;   99US-0161360.
PR   26-OCT-1999;   99US-0161361.
PR   28-OCT-1999;   99US-0161920.
PR   28-OCT-1999;   99US-0161992.
PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

  Query Match             65.5%;  Score 38;  DB 21;  Length 262;
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Qy          1 RTVVYPTMMFK 11
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Db         93 RTIIYPLRLFR 103


RESULT 4
ABB53569
ID   ABB53569 standard; Protein; 394 AA.
XX
AC   ABB53569;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Lactococcus lactis protein ycgB.
XX
KW   Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX
OS   Lactococcus lactis IL1403.
XX
PN   FR2807446-A1.
XX
PD   12-OCT-2001.
XX
PF   11-APR-2000; 2000FR-0004630.
XX
PR   11-APR-2000; 2000FR-0004630.
XX
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
PI   Bolotine A,  Sorokine A,  Renault P,  Ehrlich SD;
XX
DR   WPI; 2002-043418/06.
XX
PT   New nucleotide sequence useful in the identification or Lactococcus
PT   lactis and related species -
XX
PS   Claim 6; SEQ ID No 271; 2504pp; French.
XX
CC   The present invention is related to a Lactococcus lactis nucleotide
CC   sequence (ABA90521) and related proteins (ABB53300-ABB55621). The
CC   nucleic acid sequence is useful in the detection and/or amplification of
CC   nucleic acid sequence, particularly to identify Lactococcus lactis or
CC   related species. The proteins of the invention are useful for the
CC   biosynthesis or biodegradation of a composition of interest. The
CC   invention helps research in lactic bacteria, particularly useful in the
CC   production of yogurt and cheese.
CC   Note: The sequence data for this patent is based on equivalent patent
CC   WO200177334 (published 18-OCT-2001) which is available in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   394 AA;

  Query Match             65.5%;  Score 38;  DB 23;  Length 394;
  Best Local Similarity   66.7%;  Pred. No. 19;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |::|||| |
Db         47 TLIYPTMRF 55


RESULT 5
ABG29423
ID   ABG29423 standard; Protein; 560 AA.
XX
AC   ABG29423;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #29414.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS93610.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 59782; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
```

CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 560 AA;

Query Match 63.8%; Score 37; DB 22; Length 560;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
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Db 214 TLVIPTMMF 222

RESULT 6
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ID AAO10186 standard; Protein; 82 AA.
XX
AC AAO10186;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 24078.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI90117.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 24078; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 82 AA;

Query Match 62.1%; Score 36; DB 22; Length 82;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YPTMMFK 11
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Db 1 YPTMIFK 7

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AC AAG09307;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7187.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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Query Match 60.3%; Score 35; DB 21; Length 242;
Best Local Similarity 60.0%; Pred. No. 45;

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Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        186 RQLVYPTKLF 195


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ID   AAG07361 standard; Protein; 244 AA.
XX
AC   AAG07361;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 4485.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
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PR   23-MAR-1999;   99US-0125788.
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PR   29-MAR-1999;   99US-0126785.
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Query Match 60.3%; Score 35; DB 21; Length 244;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db        188 RQLVYPTKLF 197
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RESULT 9
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AC AAG61263;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 79443.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Query Match 60.3%; Score 35; DB 21; Length 244;
Best Local Similarity 60.0%; Pred. No. 45;
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Qy          1 RTVVYPTMMF 10
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Db        188 RQLVYPTKLF 197
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RESULT 10
AAY32315
ID AAY32315 standard; Protein; 246 AA.
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AC AAY32315;
XX
DT 28-FEB-2000 (first entry)

XX
DE Soybean neutral triacylglycerol lipase.
XX
KW Triacylglycerol lipase; soybean; fatty acid; seed oil;
KW vegetable oil; transgenic plant.
XX
OS Glycine max.
XX
PN WO9955883-A2.
XX
PD 04-NOV-1999.
XX
PF 29-APR-1999; 99WO-US09280.
XX
PR 30-APR-1998; 98US-0083688.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon EB, Cahoon RE, Kinney AJ, Rafalski JA;
XX
DR WPI; 2000-062036/05.
DR N-PSDB; AAZ34964.
XX
PT Novel plant triacylglycerol lipase polynucleotides used to alter the
PT level of the enzyme in transgenic plants -
XX
PS Claim 10; Page 58-59; 65pp; English.
XX
CC This sequence represents most of a soybean neutral triacylglycerol
CC lipase (TAGL), as deduced from the nucleotide sequence of isolated
CC cDNA clones (see AAZ34964). Novel acid and neutral TAGL polypeptides
CC (see AAY32301-17) and polynucleotides (see AAZ34950-66) from corn,
CC Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes
CC may be prepared recombinantly and used to raise antibodies, which
CC are used for detecting the enzymes in situ in cells or in vitro in
CC cell extracts. The polynucleotides may be used to create transgenic
CC plants in which the TAGL levels are present at higher or lower levels
CC than normal, or in cell types or developmental processes where they are
CC not normally found. This would alter the level of triacylglycerol and
CC cholesteryl esters found in those cells. Accumulation of fatty acids
CC with unusual structures may be a positive phenotype in plants used for
CC foods. In addition, it may be desirable to eliminate expression of TAGL
CC genes for certain applications. TAGL enzymes may also be useful for the
CC processing of plant seed oils and for the development of novel seed
CC oils. The TAGL enzymes can also be used as targets to facilitate the
CC design and/or identification of inhibitors of those enzymes that may be
CC useful as herbicides. This is desirable because inhibition of the
CC activity of either of the enzymes could lead to an inhibition of plant
CC growth.
XX
SQ Sequence 246 AA;

Query Match 60.3%; Score 35; DB 21; Length 246;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VVYPTMMF 10
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Db 75 ILYPTIMF 82

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AC AAG07360;
XX
DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 4484.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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Query Match 60.3%; Score 35; DB 21; Length 251;
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AC AAG61262;
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DT 18-OCT-2000 (first entry)
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.

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PF 25-FEB-2000; 2000EP-0301439.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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Db        195 RQLVYPTKLF 204
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
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XX
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PF 25-FEB-2000; 2000EP-0301439.
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Best Local Similarity 60.0%; Pred. No. 47;
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 14-OCT-1999; 99US-0159331.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 254;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
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Db 198 RQLVYPTKLF 207

RESULT 15
AAB86353
ID AAB86353 standard; Protein; 254 AA.
XX
AC AAB86353;
XX
DT 20-SEP-2001 (first entry)
XX
DE A. thaliana allene oxide cyclase protein SEQ ID 10.
XX
KW Allene oxide cyclase; jasmonic acid; plant; AOC; jasmonate biosynthesis;
KW signalling molecule; gene expression; stress response; perfume synthesis;
KW wound-induced signal cascade; defensive response; transgenic plant;
KW protease inhibitor synthesis; phytoalexin synthesis; alkaloid synthesis;
KW pathogen resistance; herbicide resistance; ultra-violet protection;
KW secondary metabolite production; male sterility; flower development;
KW seed formation; germination.
XX
OS Arabidopsis thaliana.
XX
PN WO200157224-A2.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-EP01148.
XX
PR 02-FEB-2000; 2000DE-1004468.
XX
PA (PFLA-) INST PFLANZENBIOCHEMIE.
XX
PI Ziegler J, Stenzel I, Hause B, Wasternack C;
XX
DR WPI; 2001-483438/52.
DR N-PSDB; AAH21490.
XX
PT Nucleic acid encoding plant allene oxide cyclase, useful for producing
PT transgenic plants with altered jasmonic acid synthesis, e.g. increased
PT resistance to pathogens -
XX
PS Claim 1b; Page 55-56; 66pp; German.
XX
CC This invention describes novel nucleic acids (I), encoding proteins
CC (II) with the activity of the allene oxide cyclase (AOC) involved in
CC jasmonate biosynthesis. Jasmonic acid (JA) is a signalling molecule
CC involved in: (i) altered gene expression in plants in response to
CC stress; and (ii) developmental processes. It is also an intermediate in
CC the wound-induced signal cascade and induces many defensive responses in
CC plants, including synthesis of protease inhibitors, phytoalexins,
CC alkaloids and perfumes. (I) is used: (i) to produce transgenic plants,
CC cells etc. with altered AOC activity, specifically altered resistance to
CC pathogens and herbivores, optimal plant/useful insect/pest interaction;
CC increased biomass, altered carbohydrate and nitrogen metabolism;
CC increased production of secondary metabolites (especially alkaloids
CC and/or phytoalexins), optimal ultra-violet protection; altered male
CC sterility and/or altered development, especially flower development, seed
CC formation and/or germination; (ii) for selective production of 9S/13S
CC (cis(+))-12-oxophytodienoic acid (III), a precursor of jasmonic acid
CC (JA); (iii) for isolation of homologous sequences; and (iv) to express
CC AOC in prokaryotic or eukaryotic cells or (in antisense orientation) to
CC inhibit its expression. (I) Makes possible large scale production of high
CC purity JA. (I) is very specific for production of (III) (contrast
CC non-enzymatic methods which produce mixtures of isomers) which is a
CC precursor for the natural enantiomer of JA. This sequence represents the
CC Arabidopsis thaliana AOC described in the invention.
XX
SQ Sequence 254 AA;

Query Match 60.3%; Score 35; DB 22; Length 254;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
| :|||| :|
Db 198 RQLVYPTKLF 207

RESULT 16
ABB90980
ID ABB90980 standard; Protein; 254 AA.
XX
AC ABB90980;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 191.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP09892.
XX
PR 28-AUG-2001; 2001WO-EP09892.
XX
PA (FARB) BAYER AG.
XX
PI Tietjen K, Weidler M;
XX
DR WPI; 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
XX
PS Claim 5; SEQ ID NO 191; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising

CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX
SQ Sequence 254 AA;

Query Match 60.3%; Score 35; DB 23; Length 254;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        198 RQLVYPTKLF 207
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RESULT 17
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ID AAG07359 standard; Protein; 258 AA.
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AC AAG07359;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4483.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
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PR 21-APR-1999; 99US-0130449.
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PR 03-JUN-1999; 99US-0137528.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 258;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RTVVYPTMMF 10
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Db        202 RQLVYPTKLF 211
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RESULT 18
AAG61261
ID AAG61261 standard; Protein; 258 AA.
XX
AC AAG61261;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 79441.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 258;
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Db        202 RQLVYPTKLF 211


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KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
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OS   Arabidopsis thaliana.
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PN   EP1033405-A2.
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Query Match 58.6%; Score 34; DB 21; Length 56;
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
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XX
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XX
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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Query Match 58.6%; Score 34; DB 21; Length 264;
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XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

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DR WPI; 2001-476283/51.
DR N-PSDB; AAK51462.
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PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
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PS Claim 20; Page 3215-3216; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
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GenCore version 5.1.6
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SUMMARIES

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3	38	65.5	262	4	US-08-634-475-2	Sequence 2, Appli
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5	34	58.6	591	4	US-09-352-159-46	Sequence 46, Appl
6	34	58.6	598	4	US-09-352-159-42	Sequence 42, Appl
7	33	56.9	700	4	US-08-274-121B-5	Sequence 5, Appli
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;     CITY: La Jolla
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
```

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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/634,475
;      FILING DATE:  18-APR-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07251/015001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-634-475-3

  Query Match             65.5%;  Score 38;  DB 4;  Length 246;
  Best Local Similarity   45.5%;  Pred. No. 8.3;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         77 RTIIYPLRLFR 87


RESULT 2
US-09-709-791-3
; Sequence 3, Application US/09709791
; Patent No. 6352846
;   GENERAL INFORMATION:
;        APPLICANT: Chory, Joanne
;                   Li, Jianming
;        TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
;                            DET2
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
;             STREET: 620 Newport Center Drive, 16th floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/709,791
;             FILING DATE: 07-No. 6352846-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fuller, Michael
;             REGISTRATION NUMBER: 36,516
;             REFERENCE/DOCKET NUMBER: SALKINS.010DV1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/235-8550
;             TELEFAX: 619/235-0176
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 246 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: not relevant
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-709-791-3

  Query Match             65.5%;  Score 38;  DB 4;  Length 246;
  Best Local Similarity   45.5%;  Pred. No. 8.3;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         77 RTIIYPLRLFR 87


RESULT 3
US-08-634-475-2
; Sequence 2, Application US/08634475
; Patent No. 6143950
;  GENERAL INFORMATION:
;    APPLICANT:  Chory et al., Joanne
;    TITLE OF INVENTION:  NOVEL PLANT STEROID 5 alpha REDUCTASE,
;    TITLE OF INVENTION:  DET2
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/634,475
;      FILING DATE:  18-APR-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07251/015001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  262 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-634-475-2

  Query Match             65.5%;  Score 38;  DB 4;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 8.9;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 4
US-09-709-791-2
; Sequence 2, Application US/09709791
; Patent No. 6352846
;   GENERAL INFORMATION:
;        APPLICANT: Chory, Joanne
;                   Li, Jianming
;        TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
;                            DET2
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
;             STREET: 620 Newport Center Drive, 16th floor
;             CITY: Newport Beach
```

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;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/709,791
;             FILING DATE: 07-No. 6352846-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fuller, Michael
;             REGISTRATION NUMBER: 36,516
;             REFERENCE/DOCKET NUMBER: SALKINS.010DV1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/235-8550
;             TELEFAX: 619/235-0176
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 262 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: not relevant
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-709-791-2

  Query Match             65.5%;  Score 38;  DB 4;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 8.9;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 5
US-09-352-159-46
; Sequence 46, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 46
;   LENGTH: 591
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
US-09-352-159-46

  Query Match             58.6%;  Score 34;  DB 4;  Length 591;
  Best Local Similarity   55.6%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        405 TTLYPTLIF 413


RESULT 6
US-09-352-159-42
; Sequence 42, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 42
;   LENGTH: 598
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
US-09-352-159-42

  Query Match             58.6%;  Score 34;  DB 4;  Length 598;
  Best Local Similarity   55.6%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        406 TTLYPTLIF 414


RESULT 7
US-08-274-121B-5
; Sequence 5, Application US/08274121B
; Patent No. 6133034
; GENERAL INFORMATION:
;    APPLICANT:  Arne Reidar Strom
;    APPLICANT:  Inga Kaasen
;    APPLICANT:  Olaf Bay Styrvold
;    APPLICANT:  John McDougall
;    TITLE OF INVENTION:  Methods and Compositions
;    TITLE OF INVENTION:  Related To The Production
;    TITLE OF INVENTION:  of Trehalose
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calgene, Inc.
;      STREET:  1920 Fifth Street
;      CITY:  Davis
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  95616
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 2.0 MB
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.1(a)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/274,121B
;      FILING DATE:  12-JULY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/893,099
;      FILING DATE:  27-MAY-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elizabeth Lassen
;      REGISTRATION NUMBER:  31,845
;      NAME:  Donna E. Scherer
;      REGISTRATION NUMBER:  34,719
;      REFERENCE/DOCKET NUMBER:  CGNE 86(1)
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (916) 753-6313
;      TELEFAX:  (916) 753-1510
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  700 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-274-121B-5

  Query Match             56.9%;  Score 33;  DB 4;  Length 700;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              : ::|||  |
Db        672 KAIIYPTFFF 681


RESULT 8
US-09-352-159-6
; Sequence 6, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-6

  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 9
US-09-352-159-8
; Sequence 8, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-8

  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 10
US-09-352-168-6
; Sequence 6, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-168-6

  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 11
US-09-352-168-8
; Sequence 8, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-168-8
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```
  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 12
US-09-352-159-11
; Sequence 11, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-11

  Query Match             55.2%;  Score 32;  DB 4;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 13
US-09-352-168-11
; Sequence 11, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   OTHER INFORMATION: Extra lysine in the polypeptide sequence of
;   OTHER INFORMATION: K:trAPAO, 463 aa.
US-09-352-168-11

  Query Match             55.2%;  Score 32;  DB 4;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 14
US-08-959-011-3
; Sequence 3, Application US/08959011
; Patent No. 5932444
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  VACUOLAR ATPASE SUBUNIT AC45
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,011
;      FILING DATE:  Herewith
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0412 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  497984
US-08-959-011-3

  Query Match             55.2%;  Score 32;  DB 2;  Length 468;
  Best Local Similarity   87.5%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTM 8
              |||| |||
Db        244 RTVVPPTM 251


RESULT 15
US-09-352-159-21
; Sequence 21, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
```

```
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(24)
US-09-352-159-21

  Query Match             55.2%;  Score 32;  DB 4;  Length 487;
  Best Local Similarity   55.6%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        295 TTLYPTLTF 303


RESULT 16
US-09-352-168-21
; Sequence 21, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(24)
;   OTHER INFORMATION: K:trAPAO translational fusion with barley alpha
;   OTHER INFORMATION: amylase signal sequence, for expression and
;   OTHER INFORMATION: secretion of the mature trAPAO in maize.
US-09-352-168-21

  Query Match             55.2%;  Score 32;  DB 4;  Length 487;
  Best Local Similarity   55.6%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        295 TTLYPTLTF 303


RESULT 17
US-09-001-826-23
; Sequence 23, Application US/09001826A
; Patent No. 5965727
; GENERAL INFORMATION:
;  APPLICANT: SONG, HEE-SOOK
;  APPLICANT: BROTHERTON, JEFFREY E.
;  APPLICANT: WIDHOLM, JACK M.
;  TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
;  TITLE OF INVENTION: TRANSFORMATION
;  FILE REFERENCE: UI001.C1
;  CURRENT APPLICATION NUMBER: US/09/001,826A
;  CURRENT FILING DATE: 1997-12-31
;  EARLIER APPLICATION NUMBER: 08/937,739;  60/025,140
;  EARLIER FILING DATE: 1997-07-25; 1996-07-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: Macintosh Wordperfect converted to PC ASCII Text
; SEQ ID NO 23
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Nicotiana tabacum
US-09-001-826-23

  Query Match             55.2%;  Score 32;  DB 2;  Length 491;
  Best Local Similarity   71.4%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        422 RTIVFPT 428


RESULT 18
US-09-352-159-17
; Sequence 17, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 554
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(89)
US-09-352-159-17

  Query Match             55.2%;  Score 32;  DB 4;  Length 554;
  Best Local Similarity   55.6%;  Pred. No. 2.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        362 TTLYPTLTF 370


RESULT 19
US-09-352-168-17
; Sequence 17, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
```

```
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 554
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(89)
;   OTHER INFORMATION: yeast alpha mating factor secretion signal.
US-09-352-168-17

  Query Match             55.2%;  Score 32;  DB 4;  Length 554;
  Best Local Similarity   55.6%;  Pred. No. 2.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        362 TTLYPTLTF 370


RESULT 20
US-09-486-382B-2
; Sequence 2, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
;  APPLICANT: Hokko Chemical Industry Co., Ltd.
;  APPLICANT:  MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
;  TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
;  TITLE OF INVENTION:  synthase of rice, and DNAs related to said genes
;  FILE REFERENCE: 10647
;  CURRENT APPLICATION NUMBER: US/09/486,382B
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: JP 9-235049
;  PRIOR FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 577
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-09-486-382B-2

  Query Match             55.2%;  Score 32;  DB 4;  Length 577;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        508 RTIVFPT 514


RESULT 21
US-09-486-382B-13
; Sequence 13, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
;  APPLICANT: Hokko Chemical Industry Co., Ltd.
;  APPLICANT:  MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
;  TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
;  TITLE OF INVENTION:  synthase of rice, and DNAs related to said genes
;  FILE REFERENCE: 10647
;  CURRENT APPLICATION NUMBER: US/09/486,382B
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: JP 9-235049
;  PRIOR FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 577
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Modified amino acid sequence of Sequence No. 6388174 2
; Patent No. 6388174
US-09-486-382B-13

  Query Match             55.2%;  Score 32;  DB 4;  Length 577;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        508 RTIVFPT 514


RESULT 22
US-08-604-789B-3
; Sequence 3, Application US/08604789B
; Patent No. 6118047
;  GENERAL INFORMATION:
;       APPLICANT: Anderson, P.C.
;                  Chomet, P.S.
;                  Griffor, M.C.
;                  Kriz, A.L.
;       TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
;                           AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
;                           OVERPRODUCTION
;       NUMBER OF SEQUENCES: 16
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
;            STREET: P.O. Box 2938
;            CITY: Minneapolis
;            STATE: MN
;            COUNTRY: USA
;            ZIP: 55402
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/604,789B
;            FILING DATE: 19-Jan-1996
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Woessner, Warren D.
;            REGISTRATION NUMBER: 30,440
;            REFERENCE/DOCKET NUMBER: 950.026US1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (612) 373-6903
;            TELEFAX: (612) 339-3061
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 595 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-604-789B-3

  Query Match             55.2%;  Score 32;  DB 3;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 RTVVYPT 7
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Db        526 RTIVFPT 532


RESULT 23
US-09-312-721A-3
; Sequence 3, Application US/09312721A
; Patent No. 6271016
;   GENERAL INFORMATION:
;        APPLICANT: Anderson, P.C.
;                   Chomet, P.S.
;                   Griffor, M.C.
;                   Kriz, A.L.
;        TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
;                            AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
;                            OVERPRODUCTION
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
;             STREET: P.O. Box 2938
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/312,721A
;             FILING DATE: 17-May-1999
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/604,789
;             FILING DATE: 19-JAN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Woessner, Warren D.
;             REGISTRATION NUMBER: 30,440
;             REFERENCE/DOCKET NUMBER: 950.026US2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (612) 373-6903
;             TELEFAX: (612) 339-3061
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 595 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-312-721A-3

  Query Match             55.2%;  Score 32;  DB 4;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        526 RTIVFPT 532


RESULT 24
US-09-352-159-40
; Sequence 40, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
;   LENGTH: 598
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (216)...(216)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-352-159-40

  Query Match             55.2%;  Score 32;  DB 4;  Length 598;
  Best Local Similarity   55.6%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        406 TTLYPTLTF 414


RESULT 25
US-09-352-159-23
; Sequence 23, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-23

  Query Match             55.2%;  Score 32;  DB 4;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        408 TTLYPTLTF 416


Search completed: July 16, 2003, 14:38:03
Job time : 15 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2003, 14:33:19 ; Search time 27.6667 Seconds
(without alignments)
47.218 Million cell updates/sec

Title: US-09-923-716C-2
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published_Applications_AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	58.6	322	9	US-10-183-116-16	Sequence 16, Appl
2	34	58.6	322	9	US-10-079-384-4	Sequence 4, Appli
3	34	58.6	600	9	US-10-072-307-28	Sequence 28, Appl
4	34	58.6	600	9	US-10-072-307-30	Sequence 30, Appl
5	34	58.6	600	9	US-10-072-307-35	Sequence 35, Appl
6	34	58.6	600	9	US-10-072-307-37	Sequence 37, Appl
7	34	58.6	600	9	US-10-072-307-40	Sequence 40, Appl
8	34	58.6	600	9	US-10-072-307-43	Sequence 43, Appl
9	34	58.6	600	9	US-10-072-307-60	Sequence 60, Appl
10	34	58.6	600	9	US-10-072-307-64	Sequence 64, Appl
11	33	56.9	600	9	US-10-072-307-62	Sequence 62, Appl
12	33	56.9	656	9	US-09-738-626-4577	Sequence 4577, Ap
13	32	55.2	447	9	US-10-169-048-34	Sequence 34, Appl
14	32	55.2	447	9	US-10-169-048-44	Sequence 44, Appl
15	32	55.2	462	9	US-09-770-564-6	Sequence 6, Appli
16	32	55.2	462	9	US-09-770-564-8	Sequence 8, Appli
17	32	55.2	463	9	US-10-072-307-46	Sequence 46, Appl
18	32	55.2	463	9	US-10-072-307-47	Sequence 47, Appl
19	32	55.2	463	9	US-10-072-307-48	Sequence 48, Appl
20	32	55.2	463	9	US-10-072-307-50	Sequence 50, Appl
21	32	55.2	463	9	US-09-770-564-11	Sequence 11, Appl
22	32	55.2	487	9	US-09-770-564-21	Sequence 21, Appl
23	32	55.2	539	9	US-10-072-307-34	Sequence 34, Appl
24	32	55.2	554	9	US-09-770-564-17	Sequence 17, Appl
25	32	55.2	595	10	US-09-733-300-3	Sequence 3, Appli
26	32	55.2	600	9	US-10-072-307-26	Sequence 26, Appl
27	32	55.2	600	9	US-10-072-307-27	Sequence 27, Appl
28	32	55.2	600	9	US-10-072-307-29	Sequence 29, Appl
29	32	55.2	600	9	US-10-072-307-31	Sequence 31, Appl
30	32	55.2	600	9	US-10-072-307-32	Sequence 32, Appl
31	32	55.2	600	9	US-10-072-307-33	Sequence 33, Appl
32	32	55.2	600	9	US-10-072-307-36	Sequence 36, Appl
33	32	55.2	600	9	US-10-072-307-38	Sequence 38, Appl
34	32	55.2	600	9	US-10-072-307-41	Sequence 41, Appl
35	32	55.2	600	9	US-10-072-307-42	Sequence 42, Appl
36	32	55.2	600	9	US-10-072-307-44	Sequence 44, Appl
37	32	55.2	600	9	US-10-072-307-45	Sequence 45, Appl
38	32	55.2	600	9	US-10-072-307-52	Sequence 52, Appl
39	32	55.2	600	9	US-10-072-307-54	Sequence 54, Appl
40	32	55.2	600	9	US-10-072-307-56	Sequence 56, Appl
41	32	55.2	600	9	US-10-072-307-58	Sequence 58, Appl
42	32	55.2	600	9	US-10-072-307-66	Sequence 66, Appl
43	32	55.2	600	9	US-09-770-564-23	Sequence 23, Appl
44	32	55.2	692	9	US-09-770-564-19	Sequence 19, Appl
45	32	55.2	829	9	US-09-770-564-33	Sequence 33, Appl
46	32	55.2	991	9	US-09-770-564-27	Sequence 27, Appl
47	32	55.2	1000	9	US-09-770-564-25	Sequence 25, Appl
48	32	55.2	1196	9	US-09-770-564-31	Sequence 31, Appl
49	32	55.2	1205	9	US-09-770-564-29	Sequence 29, Appl
50	31	53.4	57	10	US-09-864-761-47860	Sequence 47860, A
51	31	53.4	58	9	US-09-764-891-2918	Sequence 2918, Ap
52	31	53.4	157	9	US-09-992-598-103	Sequence 103, App
53	31	53.4	157	9	US-09-989-293A-103	Sequence 103, App
54	31	53.4	157	9	US-09-989-735-103	Sequence 103, App
55	31	53.4	157	9	US-09-990-444-103	Sequence 103, App
56	31	53.4	157	9	US-09-989-730-103	Sequence 103, App
57	31	53.4	157	9	US-09-990-436-103	Sequence 103, App
58	31	53.4	157	9	US-09-991-181-103	Sequence 103, App
59	31	53.4	157	9	US-09-993-687-103	Sequence 103, App
60	31	53.4	157	9	US-09-989-734-103	Sequence 103, App
61	31	53.4	157	9	US-09-997-653-103	Sequence 103, App
62	31	53.4	157	9	US-10-174-590-90	Sequence 90, Appl
63	31	53.4	157	9	US-10-176-758-90	Sequence 90, Appl
64	31	53.4	157	9	US-10-175-737-90	Sequence 90, Appl
65	31	53.4	157	9	US-09-993-667-103	Sequence 103, App
66	31	53.4	157	9	US-10-173-706-90	Sequence 90, Appl
67	31	53.4	157	9	US-10-175-738-90	Sequence 90, Appl
68	31	53.4	157	9	US-10-175-752-90	Sequence 90, Appl
69	31	53.4	157	9	US-10-176-482-90	Sequence 90, Appl
70	31	53.4	157	9	US-10-176-757-90	Sequence 90, Appl
71	31	53.4	157	9	US-10-176-913-90	Sequence 90, Appl
72	31	53.4	157	9	US-10-180-552-90	Sequence 90, Appl
73	31	53.4	157	9	US-10-180-557-90	Sequence 90, Appl
74	31	53.4	157	9	US-09-990-438-103	Sequence 103, App
75	31	53.4	157	9	US-09-990-562-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-10-183-116-16
; Sequence 16, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CP1

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;  CURRENT APPLICATION NUMBER: US/10/183,116
;  CURRENT FILING DATE:  2002-06-26
;  PRIOR APPLICATION NUMBER: US 60/222,344
;  PRIOR FILING DATE: 2000-08-01
;  PRIOR APPLICATION NUMBER: US 60/202,027
;  PRIOR FILING DATE: 2000-05-04
;  PRIOR APPLICATION NUMBER: US 09/704,707
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: US 60/285,493
;  PRIOR FILING DATE: 2001-04-19
;  PRIOR APPLICATION NUMBER: US 09/849,869
;  PRIOR FILING DATE: 2001-05-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-183-116-16

  Query Match             58.6%;  Score 34;  DB 9;  Length 322;
  Best Local Similarity   62.5%;  Pred. No. 96;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              ::|| |||
Db         97 ILYPVMMF 104


RESULT 2
US-10-079-384-4
; Sequence 4, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
;  APPLICANT: Communi, Didier
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: 9409/2132
;  CURRENT APPLICATION NUMBER: US/10/079,384
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: US 09/885,453
;  PRIOR FILING DATE: 2001-06-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-079-384-4

  Query Match             58.6%;  Score 34;  DB 9;  Length 322;
  Best Local Similarity   62.5%;  Pred. No. 96;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              ::|| |||
Db         97 ILYPVMMF 104


RESULT 3
US-10-072-307-28
; Sequence 28, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 28
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_F7
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-28

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 4
US-10-072-307-30
; Sequence 30, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 30
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_G11
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-30

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 5
US-10-072-307-35
; Sequence 35, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
```

```
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 35
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F15C3
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-35

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 6
US-10-072-307-37
; Sequence 37, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 37
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F19F2
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-37

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 7
US-10-072-307-40
; Sequence 40, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 40
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F24F2
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-40

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 8
US-10-072-307-43
; Sequence 43, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 43
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F3B5
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-43

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 9
US-10-072-307-60
; Sequence 60, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 60
```

```
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 215
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 216
;   OTHER INFORMATION: Xaa = Gln, His
US-10-072-307-60

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 10
US-10-072-307-64
; Sequence 64, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 64
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 13
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 403
;   OTHER INFORMATION: Xaa = Val, Leu, Met
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 404
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 419
;   OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 433
;   OTHER INFORMATION: Xaa = Val, Leu, Met
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 443
;   OTHER INFORMATION: Xaa = Ter, Cys, Trp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 478
;   OTHER INFORMATION: Xaa = Leu, Ter, Ser, Trp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 489
;   OTHER INFORMATION: Xaa = Ter, Arg, Gly
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 538
;   OTHER INFORMATION: Xaa = Ter, Arg, Gly
US-10-072-307-64

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 11
US-10-072-307-62
; Sequence 62, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 62
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 187
;   OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 209
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 244
;   OTHER INFORMATION: Xaa = Glu, Asp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 262
;   OTHER INFORMATION: Xaa = Ter, Cys, Trp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 295
;   OTHER INFORMATION: Xaa = Tyr, Asn, Asp, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 299
;   OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 403
;   OTHER INFORMATION: Xaa = Val, Leu, Met
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 405
;   OTHER INFORMATION: Xaa = Ala, Thr, Pro, Ser
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 409
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```
;   OTHER INFORMATION: Xaa = Ala, Thr, Ser, Pro
US-10-072-307-62

  Query Match             56.9%;  Score 33;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 2.9e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TXLYPTLIF 416


RESULT 12
US-09-738-626-4577
; Sequence 4577, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/09/738,626
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4577
;   LENGTH: 656
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-4577

  Query Match             56.9%;  Score 33;  DB 9;  Length 656;
  Best Local Similarity   62.5%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          . 3 VVYPTMMF 10
              :: |||||
Db        307 IIMPTMMF 314


RESULT 13
US-10-169-048-34
; Sequence 34, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
;  APPLICANT: Clarke, Edna Elizabeth
;  APPLICANT:  Zhou, Liqing
;  APPLICANT:  Shea, Jacqueline Elizabeth
;  APPLICANT:  Feldman, Robert Graham
;  APPLICANT:  Holden, David William
;  TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their Use
;  FILE REFERENCE: GJE-97
;  CURRENT APPLICATION NUMBER: US/10/169,048
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: PCT/GB00/04997
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-10-169-048-34

  Query Match             55.2%;  Score 32;  DB 9;  Length 447;
  Best Local Similarity   45.5%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              :|::||  ||
Db        190 QTMIYPFTFFK 200


RESULT 14
US-10-169-048-44
; Sequence 44, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
;  APPLICANT: Clarke, Edna Elizabeth
;  APPLICANT:  Zhou, Liqing
;  APPLICANT:  Shea, Jacqueline Elizabeth
;  APPLICANT:  Feldman, Robert Graham
;  APPLICANT:  Holden, David William
;  TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their
;  FILE REFERENCE: GJE-97
;  CURRENT APPLICATION NUMBER: US/10/169,048
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: PCT/GB00/04997
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-10-169-048-44

  Query Match             55.2%;  Score 32;  DB 9;  Length 447;
  Best Local Similarity   45.5%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              :|::||   ||
Db        190 QTMIYPFTFFK 200


RESULT 15
US-09-770-564-6
; Sequence 6, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-770-564-6
```

Query Match 55.2%; Score 32; DB 9; Length 462;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278
```

RESULT 16
US-09-770-564-8
; Sequence 8, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/770,564
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/352,168
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/092,936
; PRIOR FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-770-564-8

Query Match 55.2%; Score 32; DB 9; Length 462;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278
```

RESULT 17
US-10-072-307-46
; Sequence 46, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: AP1 Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 46
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_TrH1
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-46

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279
```

RESULT 18
US-10-072-307-47
; Sequence 47, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: AP1 Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 47
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_G6
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-47

Query Match 55.2%; Score 32; DB 9; Length 463;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279
```

RESULT 19
US-10-072-307-48
; Sequence 48, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Ranjini
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: English, James
; TITLE OF INVENTION: AP1 Amine Oxidase Variants
; FILE REFERENCE: 02-10402US
; CURRENT APPLICATION NUMBER: US/10/072,307
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,918
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/300,324
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 48
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LIMS-SeqID Translation_of_H8
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-072-307-48

Query Match 55.2%; Score 32; DB 9; Length 463;

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  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 20
US-10-072-307-50
; Sequence 50, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 50
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_B6
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-50

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 21
US-09-770-564-11
; Sequence 11, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   OTHER INFORMATION: Extra lysine in the polypeptide sequence of
;   OTHER INFORMATION: K:trAPAO, 463 aa.
US-09-770-564-11

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 22
US-09-770-564-21
; Sequence 21, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(24)
;   OTHER INFORMATION: K:trAPAO translational fusion with barley alpha
;   OTHER INFORMATION: amylase signal sequence, for expression and
;   OTHER INFORMATION: secretion of the mature trAPAO in maize.
US-09-770-564-21

  Query Match             55.2%;  Score 32;  DB 9;  Length 487;
  Best Local Similarity   55.6%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        295 TTLYPTLTF 303


RESULT 23
US-10-072-307-34
; Sequence 34, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 34
;   LENGTH: 539
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F15A11
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-34

  Query Match             55.2%;  Score 32;  DB 9;  Length 539;
  Best Local Similarity   55.6%;  Pred. No. 3.9e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        347 TTLYPTLTF 355


RESULT 24
US-09-770-564-17
; Sequence 17, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 554
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(89)
;   OTHER INFORMATION: yeast alpha mating factor secretion signal.
US-09-770-564-17

  Query Match             55.2%;  Score 32;  DB 9;  Length 554;
  Best Local Similarity   55.6%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        362 TTLYPTLTF 370


RESULT 25
US-09-733-300-3
; Sequence 3, Application US/09733300
; Patent No. US20020061570A1
;   GENERAL INFORMATION:
;        APPLICANT: Anderson, P.C.
;                   Chomet, P.S.
;                   Griffor, M.C.
;                   Kriz, A.L.
;        TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
;                            AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
;                            OVERPRODUCTION
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
;             STREET: P.O. Box 2938
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/733,300
;             FILING DATE: 08-Dec-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/312,721
;             FILING DATE: 2000-09-11
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Woessner, Warren D.
;             REGISTRATION NUMBER: 30,440
;             REFERENCE/DOCKET NUMBER: 950.026US2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (612) 373-6903
;             TELEFAX: (612) 339-3061
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 595 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-733-300-3

  Query Match             55.2%;  Score 32;  DB 10;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 4.4e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        526 RTIVFPT 532


Search completed: July 16, 2003, 14:39:39
Job time : 27.6667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 20 Seconds
(without alignments)
52.874 Million cell updates/sec

Title: US-09-923-716C-2
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	70.7	333	2	S74406	hypothetical prote
2	41	70.7	974	2	T29545	hypothetical prote
3	38	65.5	262	2	C84800	3-oxo-5-alpha-ster
4	38	65.5	394	2	G86657	ABC transporter AT
5	37	63.8	395	2	H83424	hypothetical prote
6	35	60.3	180	2	D86267	T6J4.4 protein - A
7	35	60.3	435	2	E72342	pmbA-related prote
8	35	60.3	598	2	AG0890	probable arylsulfa
9	35	60.3	887	2	B96598	hypothetical prote
10	34	58.6	303	2	H84758	hypothetical prote
11	34	58.6	347	2	AD3513	channel protein vi
12	34	58.6	373	2	S17955	long-chain-fatty-a
13	34	58.6	373	2	S15161	long-chain-fatty-a
14	34	58.6	389	2	AD0478	acetylornithine de
15	34	58.6	404	2	B41317	O-antigen ligase c
16	34	58.6	404	2	AE0973	O-antigen ligase [
17	34	58.6	464	2	T50785	nucleoid DNA-bindi
18	34	58.6	674	2	D72329	hypothetical prote
19	34	58.6	711	2	A86424	unknown protein, 3
20	33.5	57.8	1724	2	T13942	UNC-13-B protein -
21	33	56.9	120	1	E69798	conserved hypothet
22	33	56.9	136	2	A90710	regulator of nucle
23	33	56.9	136	2	E85560	regulator of nucle
24	33	56.9	136	2	I57917	nucleoside diphosp
25	33	56.9	205	2	S29308	hypothetical prote
26	33	56.9	205	2	F83013	probable transcrip
27	33	56.9	221	2	AH0324	probable transport
28	33	56.9	261	2	T05447	hypothetical prote
29	33	56.9	390	2	AF3425	oxidoreductase (EC
30	33	56.9	394	2	S69870	hypothetical prote
31	33	56.9	531	2	D90453	hypothetical prote
32	33	56.9	551	2	D69282	glutamyl-tRNA synt
33	33	56.9	594	2	S00961	hypothetical prote
34	33	56.9	821	2	B75530	ATP-dependent prot
35	33	56.9	1021	2	T08601	hypothetical prote
36	33	56.9	1235	2	AC1358	ATP-dependent deox
37	33	56.9	1235	2	AC1728	ATP-dependent deox
38	32	55.2	61	1	F2RZKS	photosystem II pro
39	32	55.2	136	2	AC0578	regulator of nucle
40	32	55.2	142	2	G98072	7,8-dihydro-8-oxog
41	32	55.2	143	1	WMBE6H	transcription regu
42	32	55.2	143	2	T43976	transactivator [im
43	32	55.2	169	2	S72166	lipopolysaccharide
44	32	55.2	201	2	T07011	proteinase inhibit
45	32	55.2	203	2	E75413	conserved hypothet
46	32	55.2	214	2	G71318	hypothetical prote
47	32	55.2	214	2	D89985	hypothetical prote
48	32	55.2	214	2	T49174	hypothetical prote
49	32	55.2	283	2	T13879	maturase-like prot
50	32	55.2	283	2	AG1560	hypothetical prote
51	32	55.2	283	2	AI1202	hypothetical prote
52	32	55.2	285	2	T09308	immediate-early pr
53	32	55.2	334	2	T44163	hypothetical prote
54	32	55.2	421	2	S26246	glutamate/aspartat
55	32	55.2	458	2	A96938	polyA polymerase [
56	32	55.2	468	2	A55116	vacuolar ATPase (E
57	32	55.2	513	2	T40998	hypothetical prote
58	32	55.2	526	2	T49199	anthranilate synth
59	32	55.2	543	2	T22585	hypothetical prote
60	32	55.2	564	2	S15962	hypothetical prote
61	32	55.2	595	2	JQ1684	anthranilate synth
62	32	55.2	603	2	T11843	NADH2 dehydrogenas
63	32	55.2	620	2	T21391	hypothetical prote
64	32	55.2	1416	2	D71350	probable DNA-direc
65	32	55.2	1501	2	T29094	ribulose-bisphosph
66	32	55.2	1716	2	T14103	probable DNA-direc
67	32	55.2	3175	1	RRWVEV	genome polyprotein
68	31	53.4	80	2	A60450	hypothetical prote
69	31	53.4	95	2	B83814	Na+/H+ antiporter
70	31	53.4	104	2	T17649	hypothetical prote
71	31	53.4	105	2	T44098	hypothetical prote
72	31	53.4	142	2	G95207	MutT/nudix family
73	31	53.4	185	2	T29063	hypothetical prote
74	31	53.4	207	2	D65095	hypothetical prote
75	31	53.4	207	2	A98123	hypothetical prote

ALIGNMENTS

RESULT 1
S74406
hypothetical protein sll0456 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S74406
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74406
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-333 <KAN>
A;Cross-references: EMBL:D64001; GB:AB001339; NID:g1001102; PIDN:BAA10324.1; PID:d101
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 70.7%; Score 41; DB 2; Length 333;
Best Local Similarity 77.8%; Pred. No. 2.8;

```
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |||||::|
Db        172 TVVYPTLVF 180


RESULT 2
T29545
hypothetical protein F48C1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29545
R;Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid F48C1.
A;Reference number: Z20638
A;Accession: T29545
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-974 <GAT>
A;Cross-references: EMBL:U97015; PIDN:AAB52345.1; GSPDB:GN00019; CESP:F48C1.1
A;Experimental source: strain Bristol N2; clone F48C1
C;Genetics:
A;Gene: CESP:F48C1.1
A;Map position: 1
A;Introns: 15/2; 58/3; 110/3; 150/1; 176/1; 267/2; 296/2; 326/2; 394/3; 441/1; 550/3; 59

  Query Match             70.7%;  Score 41;  DB 2;  Length 974;
  Best Local Similarity   60.0%;  Pred. No. 8.3;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :|::|| |||
Db        851 QTIIYPPMMF 860


RESULT 3
C84800
3-oxo-5-alpha-steroid 4-dehydrogenase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: C84800
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84800
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-262 <STO>
A;Cross-references: GB:AE002093; NID:g4895180; PIDN:AAD32767.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g38050
A;Map position: 2
C;Superfamily: Caenorhabditis elegans hypothetical protein ZK1251.3

  Query Match             65.5%;  Score 38;  DB 2;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 8.2;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 4
G86657
ABC transporter ATP binding protein ycgB [imported] - Lactococcus lactis subsp. lactis (
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: G86657
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86657
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <STO>
A;Cross-references: GB:AE005176; PID:g12723123; PIDN:AAK04361.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ycgB

  Query Match             65.5%;  Score 38;  DB 2;  Length 394;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |::|||| |
Db         47 TLIYPTMRF 55


RESULT 5
H83424
hypothetical protein PA1765 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83424
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <STO>
A;Cross-references: GB:AE004602; GB:AE004091; NID:g9947739; PIDN:AAG05154.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1765

  Query Match             63.8%;  Score 37;  DB 2;  Length 395;
  Best Local Similarity   60.0%;  Pred. No. 20;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | ||||:::|
Db        292 RQVVYPSLLF 301


RESULT 6
D86267
T6J4.4 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C;Accession: D86267
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86267
A;Status: preliminary
A;Molecule type: DNA
```

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A;Residues: 1-180 <STO>
A;Cross-references: GB:AE005172; NID:g9958068; PIDN:AAG09557.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

  Query Match             60.3%;  Score 35;  DB 2;  Length 180;
  Best Local Similarity   60.0%;  Pred. No. 21;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        124 RQLVYPTKLF 133


RESULT 7
E72342
pmbA-related protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72342
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: E72342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-435 <ARN>
A;Cross-references: GB:AE001743; GB:AE000512; NID:g4981241; PIDN:AAD35809.1; PID:g498125
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0727
C;Superfamily: Escherichia coli pmbA protein

  Query Match             60.3%;  Score 35;  DB 2;  Length 435;
  Best Local Similarity   54.5%;  Pred. No. 53;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | |: ||:|:|
Db        135 RVVMVPTVMYK 145


RESULT 8
AG0890
probable arylsulfate sulfotransferase [imported] - Salmonella enterica subsp. enterica s
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AG0890
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AG0890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-598 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07717.1; PID:g16504269; GSPDB:GN00176
C;Genetics:
A;Gene: STY3370

  Query Match             60.3%;  Score 35;  DB 2;  Length 598;
  Best Local Similarity   66.7%;  Pred. No. 73;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              :|:|| |||
Db        590 LVHPTQMFK 598


RESULT 9
B96598
hypothetical protein T5A14.3 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96598
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-887 <STO>
A;Cross-references: GB:AE005173; NID:g4204259; PIDN:AAD10640.1; GSPDB:GN00141
C;Genetics:
A;Gene: T5A14.3
A;Map position: 1

  Query Match             60.3%;  Score 35;  DB 2;  Length 887;
  Best Local Similarity   70.0%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              ||| ||:| |
Db        696 TVVNPTLMLK 705


RESULT 10
H84758
hypothetical protein At2g34620 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84758
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84758
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <STO>
A;Cross-references: GB:AE002093; NID:g3128213; PIDN:AAC26693.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g34620
A;Map position: 2

  Query Match             58.6%;  Score 34;  DB 2;  Length 303;
  Best Local Similarity   60.0%;  Pred. No. 57;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              || :||  ||
Db        120 RTELYPVFMF 129


RESULT 11
AD3513
channel protein virB6 homolog [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
```

```
C;Accession: AD3513
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AD3513
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53271.1; PID:g17984152; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0030
A;Map position: II

  Query Match             58.6%;  Score 34;  DB 2;  Length 347;
  Best Local Similarity   60.0%;  Pred. No. 65;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |:| | ||:|
Db        257 TIVMPYMMYK 266


RESULT 12
S17955
long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium lei
C;Species: Photobacterium leiognathi
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 03-Jun-2002
C;Accession: S17955
R;Lee, C.Y.; Szittner, R.B.; Meighen, E.A.
Eur. J. Biochem. 201, 161-167, 1991
A;Title: The lux genes of the luminous bacterial symbiont, Photobacterium leiognathi, of
coli.
A;Reference number: S17836; MUID:92007870; PMID:1915359
A;Accession: S17955
A;Molecule type: DNA
A;Residues: 1-373 <LEE>
A;Cross-references: EMBL:M63594; NID:g150687; PIDN:AAA25620.1; PID:g150692
C;Genetics:
A;Gene: luxE
C;Keywords: acid-thiol ligase
F;364/Active site: Cys (covalent substrate-binding) #status predicted

  Query Match             58.6%;  Score 34;  DB 2;  Length 373;
  Best Local Similarity   75.0%;  Pred. No. 70;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              |:|| |||
Db         78 VFPTSMFK 85


RESULT 13
S15161
long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium pho
N;Alternate names: acyl-protein synthetase
C;Species: Photobacterium phosphoreum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
C;Accession: S15161
R;Soly, R.R.; Meighen, E.A.
J. Mol. Biol. 219, 69-77, 1991
A;Title: Identification of the acyl transfer site of fatty acyl-protein synthetase from
A;Reference number: S15160; MUID:91218179; PMID:2023262
A;Accession: S15161
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-373 <JMO>
C;Genetics:
A;Gene: luxE
C;Keywords: acid-thiol ligase
F;364/Active site: Cys (covalent substrate-binding) #status predicted

  Query Match             58.6%;  Score 34;  DB 2;  Length 373;
  Best Local Similarity   75.0%;  Pred. No. 70;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              |:|| |||
Db         78 VFPTSMFK 85


RESULT 14
AD0478
acetylornithine deacetylase (EC 3.5.1.16) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
C;Accession: AD0478
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0478
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC93392.1; PID:g15981838; GSPDB:GN00175
C;Genetics:
A;Gene: argE
C;Superfamily: succinyl-diaminopimelate desuccinylase
C;Keywords: hydrolase

  Query Match             58.6%;  Score 34;  DB 2;  Length 389;
  Best Local Similarity   66.7%;  Pred. No. 73;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |: |||| |
Db        238 TIPYPTMNF 246


RESULT 15
B41317
O-antigen ligase complex protein rfaL - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 08-Oct-1999
C;Accession: B41317
R;MacLachlan, P.R.; Kadam, S.K.; Sanderson, K.E.
J. Bacteriol. 173, 7151-7163, 1991
A;Title: Cloning, characterization, and DNA sequence of the rfaLK region for lipopoly
A;Reference number: A41317; MUID:92041612; PMID:1657881
A;Accession: B41317
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <MAC>
A;Cross-references: GB:M73826; NID:g154328; PIDN:AAA27206.1; PID:g154330
C;Keywords: transmembrane protein

  Query Match             58.6%;  Score 34;  DB 2;  Length 404;
  Best Local Similarity   63.6%;  Pred. No. 76;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | |||  ||
Db        305 RVVDYPTWTFK 315


RESULT 16
AE0973
O-antigen ligase [imported] - Salmonella enterica subsp. enterica serovar Typhi (stra
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
```

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C;Accession: AE0973
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AE0973
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03281.1; PID:g16504902; GSPDB:GN00176
C;Genetics:
A;Gene: waaL

  Query Match             58.6%;  Score 34;  DB 2;  Length 404;
  Best Local Similarity   63.6%;  Pred. No. 76;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | |||  ||
Db        305 RVVDYPTWTFK 315


RESULT 17
T50785
nucleoid DNA-binding protein cnd41-like protein - Arabidopsis thaliana
N;Alternate names: protein T30N20_30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50785
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25240
A;Accession: T50785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <BEV>
A;Cross-references: EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
C;Genetics:
A;Map position: 5
A;Introns: 58/1
A;Note: T30N20_30

  Query Match             58.6%;  Score 34;  DB 2;  Length 464;
  Best Local Similarity   66.7%;  Pred. No. 88;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              || |||: |
Db        392 TVTYPTIAF 400


RESULT 18
D72329
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72329
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72329
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-674 <ARN>
A;Cross-references: GB:AE001749; GB:AE000512; NID:g4981346; PIDN:AAD35899.1; PID:g498134
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0817

  Query Match             58.6%;  Score 34;  DB 2;  Length 674;
  Best Local Similarity   60.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :| |||  ||
Db        192 QTFVYPVFMF 201


RESULT 19
A86424
unknown protein, 35070-37205 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86424
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-711 <STO>
A;Cross-references: GB:AE005172; NID:g10092467; PIDN:AAG12869.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

  Query Match             58.6%;  Score 34;  DB 2;  Length 711;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |:|||: :
Db        461 RRVIYPTLRY 470


RESULT 20
T13942
UNC-13-B protein - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13942
R;Xu, X.Z.; Wes, P.D.; Chen, H.; Li, H.S.; Yu, M.; Morgan, S.; Liu, Y.; Montell, C.
J. Biol. Chem. 273, 31297, 1998
A;Title: Retinal targets for calmodulin include proteins implicated in synaptic trans
A;Reference number: Z17709; MUID:99030403; PMID:9813038
A;Accession: T13942
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1724 <XUX>
A;Cross-references: EMBL:Y17922; NID:g3893112; PIDN:CAA76942.1; PID:g3893113
C;Genetics:
A;Cross-references: FlyBase:FBgn0025726
A;Note: UNC-13-B
C;Superfamily: protein kinase C zinc-binding repeat homology
F;602-651/Domain: protein kinase C zinc-binding repeat homology <KZN>

  Query Match             57.8%;  Score 33.5;  DB 2;  Length 1724;
  Best Local Similarity   50.0%;  Pred. No. 4.2e+02;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    5;  Gaps    1;

Qy          1 RTVVYP-----TMMFK 11
              :|:| |     |||||
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Db       1437 KTIVLPPMTDKTMMFK 1452

RESULT 21
E69798
conserved hypothetical protein yetH - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: E69798
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69798
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-120 <KUN>
A;Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12535.1; PID:g2633029
A;Experimental source: strain 168
C;Genetics:
A;Gene: yetH
C;Superfamily: Bacillus probable methylglyoxalase yurT

  Query Match             56.9%;  Score 33;  DB 1;  Length 120;
  Best Local Similarity   54.5%;  Pred. No. 34;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | |:||  | |
Db         53 RLVIYPKAMMK 63


RESULT 22
A90710
regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157:H7
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: A90710
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A90710
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34072.1; PID:g13360107; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0649

  Query Match             56.9%;  Score 33;  DB 2;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 23
E85560
regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E85560
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85560
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <STO>
A;Cross-references: GB:AE005174; NID:g12513506; PIDN:AAG54945.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: rnk

  Query Match             56.9%;  Score 33;  DB 2;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 24
I57917
nucleoside diphosphate kinase regulator - Escherichia coli (strain K-12)
N;Alternate names: rnk protein
C;Species: Escherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 01-Mar-2002
C;Accession: I57917; H64794
R;Schlictman, D.; Shankar, S.; Chakrabarty, A.M.
Mol. Microbiol. 16, 309-320, 1995
A;Title: The Escherichia coli genes sspA and rnk can functionally replace the Pseudom
A;Reference number: I57917; MUID:96015444; PMID:7565093
A;Accession: I57917
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-136 <RES>
A;Cross-references: GB:L37900; NID:g598117; PIDN:AAC36933.1; PID:g598118
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64794
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-136 <BLAT>
A;Cross-references: GB:AE000166; GB:U00096; NID:g1786819; PIDN:AAC73711.1; PID:g17868
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: rnk

  Query Match             56.9%;  Score 33;  DB 2;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 25
S29308
hypothetical protein 3 (phaC2 3' region) - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999
```

C;Accession: S29308; S28380
R;Timm, A.; Steinbuechel, A.
Eur. J. Biochem. 209, 15-30, 1992
A;Title: Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid) gene locus c
A;Reference number: S29303; MUID:93011120; PMID:1396693
A;Accession: S29308
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <TIM>
A;Cross-references: EMBL:X66592; NID:g45388; PIDN:CAA47154.1; PID:g45394

Query Match 56.9%; Score 33; DB 2; Length 205;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RTVVYPTMM 9
              ||||| ||
Db        172 RTVVYQIMM 180
```

Search completed: July 16, 2003, 14:34:16
Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 10.3333 Seconds
(without alignments)
44.152 Million cell updates/sec

Title: US-09-923-716C-2
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	38	65.5	262	1	DET2_ARATH	Q38944	arabidopsis
2	34	58.6	373	1	LUXE_PHOLE	P29334	photobacter
3	34	58.6	404	1	RFAL_SALTY	P26471	salmonella
4	33	56.9	136	1	RNK_ECOLI	P40679	escherichia
5	33	56.9	193	1	RCF1_DICDI	O96390	dictyosteli
6	33	56.9	551	1	SYE_ARCFU	O29979	archaeoglob
7	33	56.9	594	1	YKP3_KLULA	P05469	kluyveromyc
8	32	55.2	61	1	PSBK_ORYSA	P12162	oryza sativ
9	32	55.2	61	1	PSBK_WHEAT	P58273	triticum ae
10	32	55.2	143	1	B701_HSV6G	P30024	human herpe
11	32	55.2	169	1	COAD_CHRVI	P71154	chromatium
12	32	55.2	200	1	CAKB_COTJA	Q98855	coturnix co
13	32	55.2	201	1	IP23_LYCES	Q43502	lycopersico
14	32	55.2	214	1	Y473_TREPA	O83486	treponema p
15	32	55.2	421	1	GLTT_BACCA	P24944	bacillus ca
16	32	55.2	468	1	VAS1_BOVIN	P40682	bos taurus
17	32	55.2	595	1	TRPE_ARATH	P32068	arabidopsis
18	32	55.2	603	1	NU5M_HYLLA	P03919	hylobates l
19	32	55.2	1416	1	RPOC_TREPA	O83270	treponema p
20	32	55.2	1716	1	RPA1_RAT	O54889	rattus norv
21	32	55.2	3175	1	RPOA_EAV	P19811	equine arte
22	31	53.4	157	1	SMP1_HUMAN	O95807	homo sapien
23	31	53.4	207	1	YQJI_ECOLI	Q46872	escherichia
24	31	53.4	320	1	DNC_HUMAN	Q9hc21	homo sapien
25	31	53.4	362	1	MSP1_YEAST	P28737	saccharomyc
26	31	53.4	421	1	GLTT_BACST	P24943	bacillus st
27	31	53.4	437	1	SECY_BUCAI	P57571	buchnera ap
28	31	53.4	439	1	RHG1_HUMAN	Q07960	homo sapien
29	31	53.4	440	1	AK_CHLPN	Q9z610	chlamydia p
30	31	53.4	442	1	SECY_SYNY3	P77964	synechocyst
31	31	53.4	507	1	PDI_DATGL	Q9xf61	datisca glo
32	31	53.4	527	1	KITH_HSVSA	P21293	herpesvirus
33	31	53.4	601	1	NU5M_DASNO	O21335	dasypus nov
34	31	53.4	604	1	NU5M_HORSE	P48656	equus cabal
35	31	53.4	606	1	NU5M_BOVIN	P03920	bos taurus
36	31	53.4	606	1	NU5M_CERSI	O03205	ceratotheri
37	31	53.4	606	1	NU5M_EQUAS	P92485	equus asinu
38	31	53.4	606	1	NU5M_SHEEP	O78756	ovis aries
39	31	53.4	640	1	GIDA_ANASP	Q8yr87	anabaena sp
40	31	53.4	657	1	UVRB_CAMJE	Q9ppm7	campylobact
41	31	53.4	714	1	PBPF_BACSU	P38050	bacillus su
42	31	53.4	1067	1	EG52_XENLA	Q91783	xenopus lae
43	31	53.4	3358	1	PGCV_MOUSE	Q62059	mus musculu
44	31	53.4	4196	1	DYHC_SCHPO	O13290	schizosacch
45	30.5	52.6	1968	1	RRPO_PVMR	P17965	potato viru
46	30	51.7	61	1	PSBK_HORVU	P25877	hordeum vul
47	30	51.7	116	1	LUXE_PHOLU	P19842	photorhabdu
48	30	51.7	122	1	YJ41_YEAST	P47121	saccharomyc
49	30	51.7	149	1	YQBN_BACSU	P45930	bacillus su
50	30	51.7	158	1	IP2X_SOLTU	Q00782	solanum tub
51	30	51.7	193	1	RCF2_DICDI	Q9gps3	dictyosteli
52	30	51.7	221	1	KCY1_BORBU	O51154	borrelia bu
53	30	51.7	238	1	YG26_HAEIN	P44278	haemophilus
54	30	51.7	265	1	UL07_HSVSA	Q01028	herpesvirus
55	30	51.7	315	1	VC04_VACCV	P17370	vaccinia vi
56	30	51.7	316	1	VC04_VACCC	P21038	vaccinia vi
57	30	51.7	316	1	VC04_VARV	P34012	variola vir
58	30	51.7	352	1	GLN1_DAUCA	O22504	daucus caro
59	30	51.7	356	1	GLN1_MEDSA	P04078	medicago sa
60	30	51.7	356	1	GLN1_PHAVU	P04770	phaseolus v
61	30	51.7	356	1	GLNA_VIGAC	P32289	vigna aconi
62	30	51.7	358	1	GLNA_LACSA	P23712	lactuca sat
63	30	51.7	376	1	YG3W_YEAST	P53293	saccharomyc
64	30	51.7	378	1	LUXE_VIBHA	P14286	vibrio harv
65	30	51.7	416	1	PXN1_XENLA	P49263	xenopus lae
66	30	51.7	420	1	PUR2_LISIN	Q92ap4	listeria in
67	30	51.7	420	1	PUR2_LISMO	Q8y6c6	listeria mo
68	30	51.7	426	1	STE2_SACKL	P12384	saccharomyc
69	30	51.7	477	1	LYII_HUMAN	Q14108	homo sapien
70	30	51.7	477	1	LYII_RAT	P27615	rattus norv
71	30	51.7	497	1	YJ92_YEAST	P47158	saccharomyc
72	30	51.7	519	1	SNX2_HUMAN	O60749	homo sapien
73	30	51.7	519	1	SNX2_MOUSE	Q9cwk8	mus musculu
74	30	51.7	521	1	PEL1_SACPS	P79001	saccharomyc
75	30	51.7	536	1	CCA4_DROME	Q9ve00	drosophila

ALIGNMENTS

RESULT 1
DET2_ARATH
ID DET2_ARATH STANDARD; PRT; 262 AA.
AC Q38944; Q9SH83;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable steroid reductase DET2 (EC 1.3.99.-).
GN DET2 OR AT2G38050 OR T8P21.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=96185496; PubMed=8602526;
RA Li J., Nagpal P., Vitart V., McMorris T.C., Chory J.;
RT "A role for brassinosteroids in light-dependent development of
RT Arabidopsis.";
RL Science 272:398-401(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;

```
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RA   Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT   "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT   SSP consortium (Salk/Stanford/PGEC).";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Probably involved in a reduction step in the
CC       biosynthesis of the plant steroid, brassinolide. Defects in DET2
CC       leads to defects in light-regulated development.
CC   -!- PATHWAY: Brassinolide biosynthesis.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE STEROID 5-ALPHA REDUCTASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U53860; AAC49264.1; -.
DR   EMBL; AC007661; AAD32767.1; -.
DR   EMBL; AY045926; AAK76600.1; -.
DR   EMBL; AY079337; AAL85068.1; -.
DR   InterPro; IPR001104; Strd5A_dhC.
DR   Pfam; PF02544; Steroid_dh; 1.
DR   PROSITE; PS50244; S5A_REDUCTASE; 1.
KW   Oxidoreductase; Transmembrane.
FT   TRANSMEM     13     33       POTENTIAL.
FT   TRANSMEM     51     71       POTENTIAL.
FT   TRANSMEM    113    133       POTENTIAL.
FT   TRANSMEM    148    168       POTENTIAL.
FT   TRANSMEM    205    225       POTENTIAL.
FT   CONFLICT    198    198       C -> R (IN REF. 1).
SQ   SEQUENCE   262 AA;  30635 MW;  88291B8A8AF55664 CRC64;

  Query Match             65.5%;  Score 38;  DB 1;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 1.8;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 2
LUXE_PHOLE
ID   LUXE_PHOLE     STANDARD;      PRT;   373 AA.
AC   P29334;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE   protein synthetase).
GN   LUXE.
OS   Photobacterium leiognathi.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
OC   Photobacterium.
OX   NCBI_TaxID=658;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 25521;
RX   MEDLINE=92007870; PubMed=1915359;
RA   Lee C.Y., Szittner R.B., Meighen E.A.;
RT   "The lux genes of the luminous bacterial symbiont, Photobacterium
RT   leiognathi, of the ponyfish. Nucleotide sequence, difference in gene
RT   organization, and high expression in mutant Escherichia coli.";
RL   Eur. J. Biochem. 201:161-167(1991).
CC   -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC       IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC       FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC       SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC   -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC       an acyl-protein thiolester.
CC   -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M63594; AAA25620.1; -.
DR   PIR; S17955; S17955.
KW   Luminescence; Ligase.
SQ   SEQUENCE   373 AA;  43099 MW;  1B31848B00BF9921 CRC64;

  Query Match             58.6%;  Score 34;  DB 1;  Length 373;
  Best Local Similarity   75.0%;  Pred. No. 17;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              |:|| |||
Db         78 VFPTSMFK 85


RESULT 3
RFAL_SALTY
ID   RFAL_SALTY     STANDARD;      PRT;   404 AA.
AC   P26471;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   O-antigen ligase.
GN   RFAL OR WAAL OR RFBT OR STM3713.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RX   MEDLINE=92041612; PubMed=1657881;
RA   Maclachlan P.R., Kadam S.K., Sanderson K.E.;
RT   "Cloning, characterization, and DNA sequence of the rfaLK region for
RT   lipopolysaccharide synthesis in Salmonella typhimurium LT2.";
RL   J. Bacteriol. 173:7151-7163(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
CC   -!- FUNCTION: ADDS THE O-ANTIGEN ON THE GLUCOSE(II) GROUP OF LPS.
CC   -!- PATHWAY: Lipopolysaccharide core biosynthesis.
```

```
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: SHOWS ALMOST NO SIMILARITY TO E.COLI RFAL.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M73826; AAA27206.1; -.
DR   EMBL; AE008872; AAL22572.1; -.
DR   PIR; B41317; B41317.
DR   StyGene; SG10340; rfaL.
KW   Lipopolysaccharide biosynthesis; Ligase; Transmembrane;
KW   Complete proteome.
FT   TRANSMEM     66     84       POTENTIAL.
FT   TRANSMEM    184    203       POTENTIAL.
FT   TRANSMEM    227    244       POTENTIAL.
SQ   SEQUENCE   404 AA;  46034 MW;  1B84F7B3C757D2AB CRC64;

  Query Match             58.6%;  Score 34;  DB 1;  Length 404;
  Best Local Similarity   63.6%;  Pred. No. 19;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | |||  ||
Db        305 RVVDYPTWTFK 315


RESULT 4
RNK_ECOLI
ID   RNK_ECOLI      STANDARD;      PRT;   136 AA.
AC   P40679;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Regulator of nucleoside diphosphate kinase.
GN   RNK OR B0610 OR Z0754 OR ECS0649.
OS   Escherichia coli, and
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562, 83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96015444; PubMed=7565093;
RA   Schlictman D., Shankar S., Chakrabarty A.M.;
RT   "The Escherichia coli genes sspA and rnk can functionally replace the
RT   Pseudomonas aeruginosa alginate regulatory gene algR2.";
RL   Mol. Microbiol. 16:309-320(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA   Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA   Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97061202; PubMed=8905232;
RA   Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA   Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA   Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA   Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA   Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA   Yano M., Horiuchi T.;
RT   "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT   corresponding to the 12.7-28.0 min region on the linkage map.";
RL   DNA Res. 3:137-155(1996).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
CC   -!- FUNCTION: RNK AND SSPA CAN FUNCTIONALLY REPLACE P.AERUGINOSA
CC       ALGINATE REGULATORY GENE ALGR2.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L37900; AAC36933.1; -.
DR   EMBL; AE000166; AAC73711.1; -.
DR   EMBL; U82598; AAB40810.1; -.
DR   EMBL; D90701; BAA35239.1; -.
DR   EMBL; D90702; BAA35248.1; -.
DR   EMBL; AE005240; AAG54945.1; -.
DR   EMBL; AP002552; BAB34072.1; -.
DR   EcoGene; EG12637; rnk.
KW   Complete proteome.
SQ   SEQUENCE   136 AA;  14927 MW;  7043926623BA5E1E CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 9.8;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 5
RCF1_DICDI
ID   RCF1_DICDI     STANDARD;      PRT;   193 AA.
AC   O96390;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   RAS-related protein racF1.
GN   RACF1.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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```
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99214006; PubMed=10198067;
RA   Rivero F., Albrecht R., Dislich H., Bracco E., Graciotti L.,
RA   Bozzaro S., Noegel A.A.;
RT   "RacF1, a novel member of the Rho protein family in Dictyostelium
RT   discoideum, associates transiently with cell contact areas,
RT   macropinosomes and phagosomes.";
RL   Mol. Biol. Cell 10:1205-1219(1999).
CC   -!- FUNCTION: MIGHT ACT IN CONCERT AND/OR SHARE FUNCTIONS WITH OTHER
CC       MEMBERS OF THE RHO FAMILY IN THE REGULATION OF A SUBSET OF
CC       CYTOSKELETAL REARRANGEMENTS THAT ARE REQUIRED FOR THESE PROCESSES.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound.
CC   -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF037042; AAD09143.1; -.
DR   HSSP; P21181; 1AM4.
DR   DictyDb; DD?????; racF1.
DR   InterPro; IPR003578; GTPase_Rho.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR001806; Ras_trnsfrmng.
DR   InterPro; IPR005225; Small_GTP.
DR   Pfam; PF00071; ras; 1.
DR   PRINTS; PR00449; RASTRNSFRMNG.
DR   SMART; SM00174; RHO; 1.
DR   TIGRFAMs; TIGR00231; small_GTP; 1.
KW   GTP-binding; Prenylation; Lipoprotein.
FT   NP_BIND      10     17       GTP (BY SIMILARITY).
FT   NP_BIND      57     61       GTP (BY SIMILARITY).
FT   NP_BIND     115    118       GTP (BY SIMILARITY).
FT   DOMAIN       32     40       EFFECTOR REGION (POTENTIAL).
FT   LIPID       190    190       GERANYL-GERANYL (BY SIMILARITY).
SQ   SEQUENCE   193 AA;  21830 MW;  206E814C823E3B2E CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 193;
  Best Local Similarity   45.5%;  Pred. No. 14;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              |:|:||  : |
Db        173 RSVIYPNKLIK 183


RESULT 6
SYE_ARCFU
ID   SYE_ARCFU      STANDARD;      PRT;   551 AA.
AC   O29979;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE   (GluRS).
GN   GLTX OR AF0260.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC   Archaeoglobaceae; Archaeoglobus.
OX   NCBI_TaxID=2234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98049343; PubMed=9389475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulphate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC       diphosphate + L-glutamyl-tRNA(Glu).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001087; AAB90966.1; -.
DR   HSSP; P00962; 1GTR.
DR   TIGR; AF0260; -.
DR   InterPro; IPR004526; GltX_arch.
DR   InterPro; IPR000924; Glu_tRNA-synt_1c.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00749; tRNA-synt_1c; 1.
DR   PRINTS; PR00987; TRNASYNTHGLU.
DR   TIGRFAMs; TIGR00463; gltX_arch; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW   Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW   Complete proteome.
FT   SITE        100    110       "HIGH" REGION.
SQ   SEQUENCE   551 AA;  64402 MW;  A985A300C6B68F2E CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 551;
  Best Local Similarity   66.7%;  Pred. No. 41;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              |||||: |:
Db        270 VVYPTLDFE 278


RESULT 7
YKP3_KLULA
ID   YKP3_KLULA     STANDARD;      PRT;   594 AA.
AC   P05469;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Hypothetical killer plasmid PGKL-2 protein 3.
OS   Kluyveromyces lactis (Yeast).
OG   Plasmid pGKl-2.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX   NCBI_TaxID=28985;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140;
RX   MEDLINE=88289339; PubMed=3041369;
RA   Tommasino S., Ricci S., Galeotti C.L.;
RT   "Genome organization of the killer plasmid pGKL2 from Kluyveromyces
RT   lactis.";
RL   Nucleic Acids Res. 16:5863-5878(1988).
CC   -!- FUNCTION: THE PRESENCE OF THE TWO LINEAR PLASMIDS, TERMED
CC       PGKL1 AND PGKL2, IN STRAINS OF KLUYVEROMYCES LACTIS CONFERS
CC       THE KILLER PHENOTYPE TO THE HOST CELL, BY PROMOTING THE
CC       SECRETION OF A TOXIN ABLE TO INHIBIT THE GROWTH OF SENSITIVE
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CC       STRAINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X07776; CAA30604.1; -.
DR   PIR; S00961; S00961.
DR   InterPro; IPR000977; DNA_ligase.
DR   Pfam; PF01068; DNA_ligase; 1.
KW   Hypothetical protein; Plasmid.
SQ   SEQUENCE   594 AA;  70527 MW;  6AE57D37618BE6B0 CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 594;
  Best Local Similarity   36.4%;  Pred. No. 45;
  Matches    4;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              |: :||:::|:
Db         80 RSTMYPSLIFR 90


RESULT 8
PSBK_ORYSA
ID   PSBK_ORYSA     STANDARD;      PRT;    61 AA.
AC   P12162;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Photosystem II reaction center protein K precursor (PSII-K).
GN   PSBK.
OS   Oryza sativa (Rice).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RX   MEDLINE=89364698; PubMed=2770692;
RA   Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA   Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA   Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura M.;
RT   "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT   intermolecular recombination between distinct tRNA genes accounts for
RT   a major plastid DNA inversion during the evolution of the cereals.";
RL   Mol. Gen. Genet. 217:185-194(1989).
CC   -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
CC       OF PHOTOSYSTEM II.
CC   -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X15901; CAA34010.1; -.
DR   PIR; JQ0203; F2RZKS.
DR   InterPro; IPR003687; PSII_PsbK.
DR   Pfam; PF02533; PsbK; 1.
KW   Photosystem II; Chloroplast.
FT   PROPEP          1      24       POTENTIAL.
FT   CHAIN          25      61       PHOTOSYSTEM II REACTION CENTER PROTEIN K.
SQ   SEQUENCE   61 AA;  6982 MW;  BBC361067C4158F5 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 61;
  Best Local Similarity   55.6%;  Pred. No. 6.9;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              :|:|||  |
Db         14 SVIYPTSFF 22


RESULT 9
PSBK_WHEAT
ID   PSBK_WHEAT     STANDARD;      PRT;    61 AA.
AC   P58273;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Photosystem II reaction center protein K precursor (PSII-K).
GN   PSBK.
OS   Triticum aestivum (Wheat).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Chinese Spring;
RA   Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shiina T.,
RA   Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
RA   Gojobori T., Murai R., Murai K., Matsuoka Y., Ohnishi Y., Tajiri H.,
RA   Tsunewaki K.;
RT   "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
RT   complete sequence and contig clones.";
RL   Plant Mol. Biol. Rep. 18:243-253(2000).
CC   -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
CC       OF PHOTOSYSTEM II.
CC   -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB042240; BAB47017.1; -.
DR   InterPro; IPR003687; PSII_PsbK.
DR   Pfam; PF02533; PsbK; 1.
KW   Photosystem II; Chloroplast.
FT   PROPEP          1      24       BY SIMILARITY.
FT   CHAIN          25      61       PHOTOSYSTEM II REACTION CENTER PROTEIN K.
SQ   SEQUENCE   61 AA;  7030 MW;  467901067C4158FD CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 61;
  Best Local Similarity   55.6%;  Pred. No. 6.9;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              :|:|||  |
Db         14 SVIYPTSFF 22


RESULT 10
B701_HSV6G
ID   B701_HSV6G     STANDARD;      PRT;   143 AA.
AC   P30024;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Transcriptional regulatory protein B701.
OS   Human herpesvirus (type 6 / strain GS) (HHV6).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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OC   Betaherpesvirinae; Roseolovirus.
OX   NCBI_TaxID=10369;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92148942; PubMed=1310766;
RA   Geng Y., Chandran B., Josephs S.F., Wood C.;
RT   "Identification and characterization of a human herpesvirus 6 gene
RT   segment that trans activates the human immunodeficiency virus type 1
RT   promoter.";
RL   J. Virol. 66:1564-1570(1992).
CC   -!- FUNCTION: MAY BE RESPONSIBLE FOR MOST OF THE TRANS-ACTIVATING
CC       ACTIVITY ON THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROMOTER BY
CC       HHV-6. IT MAY FUNCTION BY DIRECTLY BINDING TO THE NF-KAPPAB
CC       SITE OR MAY INVOLVE CELLULAR FACTORS, SUCH AS NF-KAPPAB, EITHER
CC       DIRECTLY OR INDIRECTLY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M81789; -; NOT_ANNOTATED_CDS.
DR   PIR; A42186; WMBE6H.
KW   Transcription regulation; Trans-acting factor; Activator.
SQ   SEQUENCE   143 AA;  16385 MW;  D0CE4D7C2422AAD8 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 143;
  Best Local Similarity   50.0%;  Pred. No. 17;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :|::||  ||
Db         50 KTLLYPKTMF 59


RESULT 11
COAD_CHRVI
ID   COAD_CHRVI     STANDARD;      PRT;   169 AA.
AC   P71154;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Pantetheine-
DE   phosphate adenylyltransferase) (PPAT) (Dephospho-CoA
DE   pyrophosphorylase).
GN   COAD OR KDTB.
OS   Chromatium vinosum.
OC   Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
OC   Allochromatium.
OX   NCBI_TaxID=1049;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=D / ATCC 17899 / DSM 180;
RX   MEDLINE=96328257; PubMed=8765743;
RA   Moulis J.M.;
RT   "Molecular cloning and expression of the gene encoding Chromatium
RT   vinosum 2[4Fe-4S] ferredoxin.";
RL   Biochim. Biophys. Acta 1308:12-14(1996).
CC   -!- FUNCTION: REVERSIBLY TRANSFERS AN ADENYLYL GROUP FROM ATP TO 4'-
CC       PHOSPHOPANTETHEINE, YIELDING DEPHOSPHO-COA (DPCOA) AND
CC       PYROPHOSPHATE (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + pantetheine 4'-phosphate = diphosphate +
CC       dephospho-CoA.
CC   -!- PATHWAY: Coenzyme A (CoA) biosynthesis; fourth step.
CC   -!- SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE COAD FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U45327; AAC44332.1; -.
DR   HSSP; P23875; 1B6T.
DR   InterPro; IPR004821; Cyt_tran_rel.
DR   InterPro; IPR004820; Cytidylyltransf.
DR   InterPro; IPR001980; LPS_biosynth.
DR   Pfam; PF01467; Cytidylyltransf; 1.
DR   PRINTS; PR01020; LPSBIOSNTHSS.
DR   TIGRFAMs; TIGR00125; cyt_tran_rel; 1.
KW   Transferase; Nucleotidyltransferase; Coenzyme A biosynthesis.
SQ   SEQUENCE   169 AA;  18559 MW;  5126FD2BF32824AC CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 169;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYP 6
              ||||||
Db          2 RTVVYP 7


RESULT 12
CAKB_COTJA
ID   CAKB_COTJA     STANDARD;      PRT;   200 AA.
AC   Q98855;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Putative calcium-activated potassium channel beta subunit.
GN   CO6.
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97224079; PubMed=9070660;
RA   Oberst C., Weiskirchen R., Hartl M., Bister K.;
RT   "Suppression in transformed avian fibroblasts of a gene (CO6)
RT   encoding a membrane protein related to mammalian potassium channel
RT   regulatory subunits.";
RL   Oncogene 14:1109-1116(1997).
CC   -!- FUNCTION: POTASSIUM CHANNEL PROTEIN WHICH MAY MODULATE THE
CC       PROPERTIES OF THE PORE-FORMING ALPHA SUBUNIT (BY SIMILARITY).
CC   -!- SUBUNIT: THE CALCIUM-ACTIVATED POTASSIUM CHANNEL IS COMPOSED OF
CC       AT LEAST TWO SUBUNITS: A PORE-FORMING ALPHA SUBUNIT AND A
CC       REGULATORY BETA SUBUNIT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U67865; AAC26967.1; -.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Ionic channel; Transmembrane; Glycoprotein.
FT   TRANSMEM     20     40       POTENTIAL.
FT   TRANSMEM    167    187       POTENTIAL.
FT   CARBOHYD     89     89       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   200 AA;  22677 MW;  B7A612D8973F711F CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 200;
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  Best Local Similarity   55.6%;  Pred. No. 23;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | ::||:||
Db        169 TFLWPTLMF 177


RESULT 13
IP23_LYCES
ID   IP23_LYCES     STANDARD;      PRT;   201 AA.
AC   Q43502;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Proteinase inhibitor type II CEVI57 precursor.
GN   CEVI57.
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4081;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Rutgers; TISSUE=Leaf;
RX   MEDLINE=96252900; PubMed=8672818;
RA   Gadea J., Mayda E., Conejero V., Vera P.;
RT   "Characterization of defense-related genes ectopically expressed in
RT   viroid-infected tomato plants.";
RL   Mol. Plant Microbe Interact. 9:409-415(1996).
CC   -!- INDUCTION: BY VIROID INFECTION.
CC   -!- SIMILARITY: BELONGS TO THE POTATO TYPE II PROTEINASE INHIBITOR
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X94946; CAA64416.1; -.
DR   HSSP; P01080; 4SGB.
DR   InterPro; IPR003465; Prot_inhib.
DR   Pfam; PF02428; Prot_inhib_II; 3.
KW   Serine protease inhibitor; Repeat; Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    201       PROTEINASE INHIBITOR TYPE II CEVI57.
FT   REPEAT       27     83       1.
FT   REPEAT       84    143       2.
FT   REPEAT      144    199       3.
FT   ACT_SITE     32     33       INTERACTION WITH TRYPSIN (PROBABLE).
FT   ACT_SITE    147    148       INTERACTION WITH TRYPSIN (PROBABLE).
SQ   SEQUENCE   201 AA;  21419 MW;  A3FCAB93773D8590 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 201;
  Best Local Similarity   57.1%;  Pred. No. 23;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              :|::|||
Db        106 KTIIYPT 112


RESULT 14
Y473_TREPA
ID   Y473_TREPA     STANDARD;      PRT;   214 AA.
AC   O83486;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein TP0473.
GN   TP0473.
OS   Treponema pallidum.
OC   Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX   NCBI_TaxID=160;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nichols;
RX   MEDLINE=98332770; PubMed=9665876;
RA   Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA   Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA   Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA   Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA   McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA   Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA   Venter J.C.;
RT   "Complete genome sequence of Treponema pallidum, the syphilis
RT   spirochete.";
RL   Science 281:375-388(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001224; AAC65467.1; -.
DR   TIGR; TP0473; -.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM      4     23       POTENTIAL.
FT   TRANSMEM     35     57       POTENTIAL.
FT   TRANSMEM     67     89       POTENTIAL.
FT   TRANSMEM     96    118       POTENTIAL.
FT   TRANSMEM    128    150       POTENTIAL.
FT   TRANSMEM    155    177       POTENTIAL.
FT   TRANSMEM    187    209       POTENTIAL.
SQ   SEQUENCE   214 AA;  24001 MW;  1497AA7E15DFAE92 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 214;
  Best Local Similarity   66.7%;  Pred. No. 25;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||||| :|:
Db        186 RTVVYTSML 194


RESULT 15
GLTT_BACCA
ID   GLTT_BACCA     STANDARD;      PRT;   421 AA.
AC   P24944;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier
DE   protein).
GN   GLTT.
OS   Bacillus caldotenax.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1395;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93062018; PubMed=1359385;
RA   Tolner B., Poolman B., Konings W.N.;
RT   "Characterization and functional expression in Escherichia coli of
RT   the sodium/proton/glutamate symport proteins of Bacillus
RT   stearothermophilus and Bacillus caldotenax.";
RL   Mol. Microbiol. 6:2845-2856(1992).
CC   -!- FUNCTION: THIS CARRIER PROTEIN IS PART OF THE NA(+)-DEPENDENT,
CC       BINDING-PROTEIN-INDEPENDENT GLUTAMATE-ASPARTATE TRANSPORT SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
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CC   -!- SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
CC       (SDF, TC 2.A.23).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M86509; AAA22493.1; -.
DR   PIR; S26246; S26246.
DR   InterPro; IPR001991; Na/diCO_symp.
DR   Pfam; PF00375; SDF; 1.
DR   PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; 1.
DR   PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; 1.
KW   Transport; Transmembrane; Symport.
FT   DOMAIN        1      3       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      4     24       POTENTIAL.
FT   DOMAIN       25     43       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     44     64       POTENTIAL.
FT   DOMAIN       65     77       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     78     98       POTENTIAL.
FT   DOMAIN       99    148       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    149    169       POTENTIAL.
FT   DOMAIN      170    198       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    199    219       POTENTIAL.
FT   DOMAIN      220    222       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    223    243       POTENTIAL.
FT   DOMAIN      244    244       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    245    265       POTENTIAL.
FT   DOMAIN      266    306       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    307    327       POTENTIAL.
FT   DOMAIN      328    330       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    331    351       POTENTIAL.
FT   TRANSMEM    352    372       POTENTIAL.
FT   DOMAIN      373    421       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   421 AA;  45345 MW;  10ABBE12EDD1E7E4 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 421;
  Best Local Similarity   75.0%;  Pred. No. 50;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              ||| ||:|
Db        226 VVYATMLF 233


RESULT 16
VAS1_BOVIN
ID   VAS1_BOVIN     STANDARD;      PRT;   468 AA.
AC   P40682;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Vacuolar ATP synthase subunit S1 precursor (EC 3.6.3.14) (V-ATPase S1
DE   subunit) (V-ATPase S1 accessory protein) (V-ATPase Ac45 subunit).
GN   ATP6IP1 OR ATP6S1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 378-388.
RC   TISSUE=Adrenal chromaffin;
RX   MEDLINE=95014142; PubMed=7929063;
RA   Supek F., Supekova L., Mandiyan S., Pan Y.-C.E., Nelson H., Nelson N.;
RT   "A novel accessory subunit for vacuolar H(+)-ATPase from chromaffin
RT   granules.";
RL   J. Biol. Chem. 269:24102-24106(1994).
CC   -!- FUNCTION: VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY
CC       OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
CC   -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC       H(+)(Out).
CC   -!- SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U10039; AAA50752.1; -.
KW   ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
KW   Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    468       VACUOLAR ATP SYNTHASE SUBUNIT S1.
FT   TRANSMEM    418    438       POTENTIAL.
FT   CARBOHYD     167    167       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     258    258       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     271    271       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     294    294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     355    355       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     404    404       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   468 AA;  51781 MW;  BF2C42D56ABB1B6D CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 468;
  Best Local Similarity   87.5%;  Pred. No. 56;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTM 8
              |||| |||
Db        244 RTVVPPTM 251


RESULT 17
TRPE_ARATH
ID   TRPE_ARATH     STANDARD;      PRT;   595 AA.
AC   P32068;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Anthranilate synthase component I-1, chloroplast precursor
DE   (EC 4.1.3.27).
GN   ASA1 OR AT5G05730 OR MJJ3.14.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93005721; PubMed=1392592;
RA   Niyogi K.K., Fink G.R.;
RT   "Two anthranilate synthase genes in Arabidopsis: defense-related
RT   regulation of the tryptophan pathway.";
RL   Plant Cell 4:721-733(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=97471969; PubMed=9330910;
RA   Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA   Miyajima N., Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT   features of the 1.6 Mb regions covered by twenty physically assigned
RT   P1 clones.";
RL   DNA Res. 4:215-230(1997).
CC   -!- CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate +
CC       pyruvate + L-glutamate.
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CC   -!- PATHWAY: Tryptophan biosynthesis; first step.
CC   -!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II.
CC   -!- SUBCELLULAR LOCATION: Chloroplast (Probable).
CC   -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC       USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC       GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M92353; AAA32738.1; -.
DR   EMBL; AB005237; BAB09667.1; -.
DR   PIR; S27751; S27751.
DR   HSSP; Q06128; 1QDL.
DR   InterPro; IPR005256; Anth_synthI.
DR   InterPro; IPR000350; Chorismate_bind.
DR   Pfam; PF00425; chorismate_bind; 1.
DR   PRINTS; PR00095; ANTSNTHASEI.
DR   ProDom; PD000779; Chorismate_bind; 1.
DR   TIGRFAMs; TIGR00564; trpE_most; 1.
KW   Tryptophan biosynthesis; Lyase; Chloroplast; Transit peptide;
KW   Multigene family.
FT   TRANSIT       1      ?       CHLOROPLAST (POTENTIAL).
FT   CHAIN         ?    595       ANTHRANILATE SYNTHASE COMPONENT I-1.
SQ   SEQUENCE   595 AA;  66311 MW;  674175416A2726F0 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 72;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:|| 
Db        526 RTIVFPT 532


RESULT 18
NU5M_HYLLA
ID   NU5M_HYLLA     STANDARD;      PRT;   603 AA.
AC   P03919;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
GN   MTND5 OR ND5 OR NADH5.
OS   Hylobates lar (Common gibbon).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9580;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ester;
RA   Arnason U., Gullberg A., Xu X.;
RT   "A complete mitochondrial DNA molecule of the white-handed gibbon,
RT   Hylobates lar, and comparison among individual mitochondrial genes of
RT   all hominoid genera.";
RL   Hereditas 124:185-189(1996).
RN   [2]
RP   SEQUENCE OF 1-79 FROM N.A.
RX   MEDLINE=82242101; PubMed=6284948;
RA   Brown W.M., Prager E.M., Wang A., Wilson A.C.;
RT   "Mitochondrial DNA sequences of primates: tempo and mode of
RT   evolution.";
RL   J. Mol. Evol. 18:225-239(1982).
CC   -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X99256; CAA67638.1; -.
DR   EMBL; V00659; CAA24025.1; -.
DR   PIR; A00449; A00449.
DR   InterPro; IPR003916; NADHub_oxred5.
DR   InterPro; IPR001750; Oxidored_q1.
DR   InterPro; IPR001516; Oxidored_q1_N.
DR   Pfam; PF00361; oxidored_q1; 1.
DR   Pfam; PF00662; oxidored_q1_N; 1.
DR   PRINTS; PR01434; NADHDHGNASE5.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ   SEQUENCE   603 AA;  67360 MW;  3BFF99C6EA7BCE70 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 603;
  Best Local Similarity   71.4%;  Pred. No. 73;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VYPTMMF 10
              ::|||||
Db         48 LFPTMMF 54


RESULT 19
RPOC_TREPA
ID   RPOC_TREPA     STANDARD;      PRT;  1416 AA.
AC   O83270;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE   beta' chain) (RNA polymerase beta' subunit).
GN   RPOC OR TP0242.
OS   Treponema pallidum.
OC   Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX   NCBI_TaxID=160;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nichols;
RX   MEDLINE=98332770; PubMed=9665876;
RA   Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA   Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA   Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA   Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA   McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA   Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA   Venter J.C.;
RT   "Complete genome sequence of Treponema pallidum, the syphilis
RT   spirochete.";
RL   Science 281:375-388(1998).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC       ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC       BETA' CHAIN.
CC   -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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CC   ----------------------------------------------------------------------
DR   EMBL; AE001205; AAC65230.1; -.
DR   HSSP; Q9KWU6; 1HQM.
DR   TIGR; TP0242; -.
DR   InterPro; IPR000722; RNA_pol_A.
DR   InterPro; IPR002879; RNA_pol_A2.
DR   Pfam; PF00623; RNA_pol_A; 1.
DR   Pfam; PF01854; RNA_pol_A2; 2.
KW   Transferase; DNA-directed RNA polymerase; Transcription;
KW   Complete proteome.
SQ   SEQUENCE   1416 AA;  159789 MW;  78D0EB6A1CAF7C9C CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 1416;
  Best Local Similarity   71.4%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|||:
Db        486 RTIVYPS 492


RESULT 20
RPA1_RAT
ID   RPA1_RAT       STANDARD;      PRT;  1716 AA.
AC   O54889;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DNA-directed RNA polymerase I largest subunit (EC 2.7.7.6) (RNA
DE   polymerase I 194 kDa subunit) (RPA194).
GN   POLR1A OR RPO1-4 OR RPA1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98086309; PubMed=9422795;
RA   Hannan R.D., Hempel W.M., Cavanaugh A., Arino T., Dimitrov S.I.,
RA   Moss T., Rothblum L.;
RT   "Affinity purification of mammalian RNA polymerase I. Identification
RT   of an associated kinase.";
RL   J. Biol. Chem. 273:1257-1267(1998).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES. RNA POLYMERASE I IS ESSENTIALLY USED TO TRANSCRIBE
CC       RIBOSOMAL DNA UNITS.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 14
CC       DIFFERENT POLYPEPTIDES. THIS SUBUNIT IS THE LARGEST COMPONENT OF
CC       RNA POLYMERASE I.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC       FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC       PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC       III FOR 5S AND TRNA GENES.
CC   -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF025425; AAB94601.1; -.
DR   InterPro; IPR000722; RNA_pol_A.
DR   InterPro; IPR002879; RNA_pol_A2.
DR   Pfam; PF00623; RNA_pol_A; 1.
DR   Pfam; PF01854; RNA_pol_A2; 2.
KW   Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
KW   Zinc-finger; Nuclear protein.
FT   ZN_FING      64     80       C2H2-TYPE (POTENTIAL).
SQ   SEQUENCE   1716 AA;  194191 MW;  E8EE15BC23E60941 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 1716;
  Best Local Similarity   50.0%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |: || |: |
Db        224 TITYPAMVHK 233


RESULT 21
RPOA_EAV
ID   RPOA_EAV       STANDARD;      PRT;  3175 AA.
AC   P19811; Q88625;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   POL polyprotein (ORF1A/1B) [Contains: RNA-directed RNA polymerase
DE   (EC 2.7.7.48); Helicase; Protease (EC 3.4.21.-)].
GN   POL.
OS   Equine arteritis virus (EAV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC   Arteriviridae; Arterivirus.
OX   NCBI_TaxID=11047;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bucyrus;
RX   MEDLINE=91237805; PubMed=1851863;
RA   den Boon J.A., Snijder E.J., Chirnside E.D., de Vries A.A.F.,
RA   Horzinek M.C., Spaan W.J.M.;
RT   "Equine arteritis virus is not a togavirus but belongs to the
RT   coronaviruslike superfamily.";
RL   J. Virol. 65:2910-2920(1991).
RN   [2]
RP   SEQUENCE OF 1-17 FROM N.A.
RC   STRAIN=Bucyrus;
RX   MEDLINE=90287699; PubMed=2162519;
RA   de Vries A.A.F., Chirnside E.D., Bredenbeek P.J., Gravestein L.A.,
RA   Horzinek M.C., Spaan W.J.M.;
RT   "All subgenomic mRNAs of equine arteritis virus contain a common
RT   leader sequence.";
RL   Nucleic Acids Res. 18:3241-3247(1990).
CC   -!- FUNCTION: RNA-DIRECTED RNA POLYMERASE & POSSIBLE HELICASE. A
CC       ROLE FOR NTP-BINDING PROTEINS IN RNA DUPLEX UNWINDING HAS BEEN
CC       SUGGESTED. ALSO CONTAINS A PROTEASE DOMAIN.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- MISCELLANEOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
CC       FOR 1727-ASN AND 1728-LEU.
CC   -!- SIMILARITY: WITH THE POLYMERASE PROTEIN OF OTHER CORONAVIRUSES AND
CC       OF TOROVIRUSES.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S32.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X53459; CAA37539.1; ALT_SEQ.
DR   EMBL; X53459; CAA37540.1; ALT_SEQ.
DR   EMBL; X52277; CAA36520.1; -.
DR   PIR; S10158; S10158.
DR   PIR; A39925; RRWVEV.
DR   MEROPS; C31.UNW; -.
DR   MEROPS; C32.001; -.
DR   MEROPS; C33.001; -.
DR   MEROPS; S32.001; -.
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DR   InterPro; IPR000606; Viral_helicase1.
DR   Pfam; PF01443; Viral_helicase1; 1.
KW   RNA-directed RNA polymerase; Transferase; Helicase; ATP-binding;
KW   Hydrolase; Serine protease; Zinc-finger.
FT   CHAIN         1   1727       ORF1A.
FT   CHAIN      1728   3175       ORF1B.
FT   DOMAIN     1080   1220       TRYPSIN-LIKE SERINE PROTEASE.
FT   DOMAIN     1218   1506       HELICASE.
FT   DOMAIN     2098   2306       POLYMERASE.
FT   ACT_SITE   1103   1103       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   1129   1129       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   1184   1184       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ZN_FING    2368   2414       BY SIMILARITY.
FT   NP_BIND    2528   2535       ATP (BY SIMILARITY).
SQ   SEQUENCE   3175 AA;  345275 MW;  ED5C8BA0E31DE695 CRC64;

  Query Match           55.2%;  Score 32;  DB 1;  Length 3175;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 YPTMMF 10
              ||||:|
Db       1369 YPTMLF 1374


RESULT 22
SMP1_HUMAN
ID   SMP1_HUMAN     STANDARD;      PRT;   157 AA.
AC   O95807;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Small membrane protein 1.
GN   SMP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hu G.;
RT   "A new member of the 18 kDa small membrane protein family in human.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21154917; PubMed=11230166;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a catalog of human genes and proteins: sequencing and
RT   analysis of 500 novel complete protein coding human cDNAs.";
RL   Genome Res. 11:422-435(2001).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANT VAL-58.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA   Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: STRONG, TO C21ORF4.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF081282; AAD17754.1; -.
DR   EMBL; AL136627; CAB66562.1; -.
DR   EMBL; AF458851; AAL51108.1; -.
DR   MIM; 605348; -.
KW   Transmembrane; Polymorphism.
FT   TRANSMEM     26     46       POTENTIAL.
FT   TRANSMEM     58     78       POTENTIAL.
FT   TRANSMEM     95    115       POTENTIAL.
FT   TRANSMEM    126    146       POTENTIAL.
FT   VARIANT      58     58       A -> V.
FT                                /FTId=VAR_013121.
FT   VARIANT     141    141       F -> L.
FT                                /FTId=VAR_007851.
SQ   SEQUENCE   157 AA;  17400 MW;  8CDF83AA23EBB1FA CRC64;

  Query Match           53.4%;  Score 31;  DB 1;  Length 157;
  Best Local Similarity   83.3%;  Pred. No. 29;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 VVYPTM 8
              |:||||
Db         44 VIYPTM 49


RESULT 23
YQJI_ECOLI
ID   YQJI_ECOLI     STANDARD;      PRT;   207 AA.
AC   Q46872;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein yqjI.
GN   YQJI OR B3071.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U28379; AAA89150.1; -.
DR   EMBL; AE000389; AAC76106.1; -.
DR   EcoGene; EG12954; yqjI.
DR   InterPro; IPR005149; PadR.
DR   Pfam; PF03551; PadR; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   207 AA;  23401 MW;  DD3D108D83E087F7 CRC64;

  Query Match           53.4%;  Score 31;  DB 1;  Length 207;
  Best Local Similarity   62.5%;  Pred. No. 39;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              |:|||: |
Db         99 VIYPTLDF 106


RESULT 24
DNC_HUMAN
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ID   DNC_HUMAN      STANDARD;      PRT;   320 AA.
AC   Q9HC21;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling
DE   protein 1).
GN   SLC25A19 OR DNC OR MUP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   PubMed=11226231;
RA   Dolce V., Fiermonte G., Runswick M.J., Palmieri F., Walker J.E.;
RT   "The human mitochondrial deoxynucleotide carrier and its role in the
RT   toxicity of nucleoside antivirals.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Renard S., Mondesert G., Besnard F.;
RT   "MUP 1, a mitochondrial uncoupling protein.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Responsible for the uptake of deoxynucleotides into the
CC       matrix of the mitochondria. Transports all four deoxy NDPs, and,
CC       less efficiently, the corresponding dNTPs. Does not transport
CC       dNMPs, NMPs, deoxynucleosides, nucleosides, purines, or
CC       pyrimidines. Supply deoxynucleotides to the mitochondrial matrix
CC       for conversion to triphosphates and incorporation into
CC       mitochondrial DNA.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC       inner membrane.
CC   -!- TISSUE SPECIFICITY: Expressed in all tissues examined except for
CC       placenta. Highest levels in colon, kidney, lung, testis, spleen,
CC       and brain.
CC   -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC   -!- DISEASE: Likely to be medically important by providing the means
CC       of uptake into mitochondria of nucleoside analogs, leading to the
CC       mitochondrial impairment that underlies the toxic side effects of
CC       such drugs in the treatment of viral illnesses, including AIDS,
CC       and in cancer therapy.
CC   -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ251857; CAC27560.1; -.
DR   EMBL; AJ301616; CAC37793.1; -.
DR   EMBL; AF182404; AAG16903.1; -.
DR   EMBL; BC001075; AAH01075.1; -.
DR   EMBL; BC005120; AAH05120.1; -.
DR   Genew; HGNC:14409; SLC25A19.
DR   MIM; 606521; -.
DR   InterPro; IPR002067; Mit_carrier.
DR   InterPro; IPR001993; Mitoch_carrier.
DR   Pfam; PF00153; mito_carr; 3.
DR   PRINTS; PR00926; MITOCARRIER.
DR   PROSITE; PS00215; MITOCH_CARRIER; 2.
KW   Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT   TRANSMEM     19     39       POTENTIAL.
FT   TRANSMEM     87    107       POTENTIAL.
FT   TRANSMEM    122    142       POTENTIAL.
FT   TRANSMEM    173    193       POTENTIAL.
FT   TRANSMEM    293    313       POTENTIAL.
SQ   SEQUENCE   320 AA;  35511 MW;  57CE0F01D538B1BE CRC64;

  Query Match             53.4%;  Score 31;  DB 1;  Length 320;
  Best Local Similarity   45.5%;  Pred. No. 61;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              :|: ||  :||
Db        231 KTLTYPLDLFK 241


RESULT 25
MSP1_YEAST
ID   MSP1_YEAST     STANDARD;      PRT;   362 AA.
AC   P28737;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   MSP1 protein (TAT-binding homolog 4).
GN   MSP1 OR YTA4 OR YGR028W.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SF747-19D;
RX   MEDLINE=94043260; PubMed=8226973;
RA   Nakai M., Endo T., Hase T., Matsubara H.;
RT   "Intramitochondrial protein sorting. Isolation and characterization
RT   of the yeast MSP1 gene which belongs to a novel family of putative
RT   ATPases.";
RL   J. Biol. Chem. 268:24262-24269(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RX   MEDLINE=95274317; PubMed=7754704;
RA   Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehnle S.,
RA   Schwarzlose C., Vetter I., Feldmann H.;
RT   "Identification of a set of yeast genes coding for a novel family of
RT   putative ATPases with high similarity to constituents of the 26S
RT   protease complex.";
RL   Yeast 10:1141-1155(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RX   MEDLINE=97435481; PubMed=9290212;
RA   Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
RT   "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
RT   chromosome VII.";
RL   Yeast 13:1077-1090(1997).
RN   [4]
RP   SEQUENCE OF 280-362 FROM N.A.
RC   STRAIN=SC167;
RX   MEDLINE=92204135; PubMed=1552903;
RA   Lisowsky T.;
RT   "Dual function of a new nuclear gene for oxidative phosphorylation
RT   and vegetative growth in yeast.";
RL   Mol. Gen. Genet. 232:58-64(1992).
CC   -!- FUNCTION: INVOLVED IN INTRAMITOCHONDRIAL SORTING OF PROTEINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC       outer membrane.
CC   -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X68055; CAA48191.1; -.
DR   EMBL; X81069; CAA56956.1; -.
DR   EMBL; Z72813; CAA97015.1; -.
DR   EMBL; X60722; -; NOT_ANNOTATED_CDS.
DR   PIR; S20468; S20468.
DR   PIR; S37410; S37410.
DR   SGD; S0003260; MSP1.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003959; AAA_ATPase_centr.
DR   InterPro; IPR003960; AAA_sub.
DR   Pfam; PF00004; AAA; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00674; AAA; 1.
KW   ATP-binding; Mitochondrion; Outer membrane; Transmembrane.
FT   DOMAIN        1     12       INTERMEMBRANE (POTENTIAL).
FT   TRANSMEM     13     28       POTENTIAL.
FT   DOMAIN       29    362       CYTOPLASMIC (POTENTIAL).
FT   NP_BIND     133    140       ATP (POTENTIAL).
SQ   SEQUENCE   362 AA;  40343 MW;  1B3562A32F47F434 CRC64;

  Query Match             53.4%;  Score 31;  DB 1;  Length 362;
  Best Local Similarity   62.5%;  Pred. No. 69;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMM 9
              :|:|| ||
Db        106 SVIYPLMM 113


Search completed: July 16, 2003, 14:35:15
Job time : 27.3333 secs
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:45 ; Search time 41.6667 Seconds
(without alignments)
54.396 Million cell updates/sec

Title: US-09-923-716C-2
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	70.7	333	16	Q55184	Q55184 synechocyst
2	41	70.7	974	5	O01574	O01574 caenorhabdi
3	38	65.5	394	16	Q9CIU3	Q9ciu3 lactococcus
4	37	63.8	390	10	Q8VWX1	Q8vwx1 perilla fru
5	37	63.8	391	10	Q9ZPP7	Q9zpp7 perilla fru
6	37	63.8	395	16	Q9I2X4	Q9i2x4 pseudomonas
7	36	62.1	512	10	Q9LUC5	Q9luc5 arabidopsis
8	35	60.3	180	10	Q9FX69	Q9fx69 arabidopsis
9	35	60.3	254	10	Q93ZC5	Q93zc5 arabidopsis
10	35	60.3	258	10	Q9LS01	Q9ls01 arabidopsis
11	35	60.3	264	16	Q8ZLZ1	Q8zlz1 salmonella
12	35	60.3	282	10	Q94JV3	Q94jv3 arabidopsis
13	35	60.3	320	11	Q8VGS2	Q8vgs2 mus musculu
14	35	60.3	435	16	Q9WZI6	Q9wzi6 thermotoga
15	35	60.3	504	12	Q9EME6	Q9eme6 amsacta moo
16	35	60.3	598	16	Q8Z3N6	Q8z3n6 salmonella
17	35	60.3	705	5	Q8SWA5	Q8swa5 encephalito
18	35	60.3	733	10	Q8S7E2	Q8s7e2 oryza sativ
19	35	60.3	735	10	Q9FJR9	Q9fjr9 arabidopsis
20	35	60.3	887	10	Q9ZVV2	Q9zvv2 arabidopsis
21	35	60.3	1030	3	Q9HFQ9	Q9hfq9 emericella
22	34	58.6	54	12	Q84121	Q84121 influenzavi
23	34	58.6	173	13	Q8UUZ6	Q8uuz6 brachydanio
24	34	58.6	180	16	Q98ID0	Q98id0 rhizobium l
25	34	58.6	212	16	Q8XNC4	Q8xnc4 clostridium
26	34	58.6	217	17	Q9HHU4	Q9hhu4 halobacteri
27	34	58.6	303	10	O64685	O64685 arabidopsis
28	34	58.6	316	10	Q9LSV4	Q9lsv4 arabidopsis
29	34	58.6	320	17	Q8U223	Q8u223 pyrococcus
30	34	58.6	322	4	Q96LB2	Q96lb2 homo sapien
31	34	58.6	322	4	Q8TDD9	Q8tdd9 homo sapien
32	34	58.6	322	4	Q8TDD8	Q8tdd8 homo sapien
33	34	58.6	347	2	Q9KIS7	Q9kis7 brucella ab
34	34	58.6	347	16	Q8YDZ2	Q8ydz2 brucella me
35	34	58.6	373	2	P95523	P95523 photobacter
36	34	58.6	373	2	Q52100	Q52100 photobacter
37	34	58.6	389	16	Q8ZA85	Q8za85 yersinia pe
38	34	58.6	404	16	Q8Z2F8	Q8z2f8 salmonella
39	34	58.6	464	10	Q9LEW3	Q9lew3 arabidopsis
40	34	58.6	530	17	Q973Z9	Q973z9 sulfolobus
41	34	58.6	674	16	Q9WZS4	Q9wzs4 thermotoga
42	34	58.6	711	10	Q9C8R8	Q9c8r8 arabidopsis
43	33.5	57.8	1304	5	O96959	O96959 drosophila
44	33.5	57.8	1508	5	Q8T049	Q8t049 drosophila
45	33.5	57.8	1724	5	O96960	O96960 drosophila
46	33.5	57.8	1752	5	Q9U4K9	Q9u4k9 drosophila
47	33.5	57.8	1810	5	Q9V483	Q9v483 drosophila
48	33	56.9	120	16	O31535	O31535 bacillus su
49	33	56.9	159	8	Q950X8	Q950x8 tetrahymena
50	33	56.9	205	2	Q51516	Q51516 pseudomonas
51	33	56.9	205	16	Q9HUC4	Q9huc4 pseudomonas
52	33	56.9	221	16	Q8ZDB7	Q8zdb7 yersinia pe
53	33	56.9	237	10	Q8RX02	Q8rx02 arabidopsis
54	33	56.9	261	10	Q9SUW6	Q9suw6 arabidopsis
55	33	56.9	299	4	Q9NXA8	Q9nxa8 homo sapien
56	33	56.9	310	4	Q9Y6E6	Q9y6e6 homo sapien
57	33	56.9	390	16	Q8YFX4	Q8yfx4 brucella me
58	33	56.9	457	17	Q9HLH0	Q9hlh0 thermoplasm
59	33	56.9	457	17	Q978Q5	Q978q5 thermoplasm
60	33	56.9	474	10	Q43541	Q43541 lilium long
61	33	56.9	531	17	Q97V62	Q97v62 sulfolobus
62	33	56.9	703	12	Q83467	Q83467 porcine ade
63	33	56.9	725	5	Q9VD08	Q9vd08 drosophila
64	33	56.9	821	16	Q9RXG4	Q9rxg4 deinococcus
65	33	56.9	842	17	Q970B4	Q970b4 sulfolobus
66	33	56.9	1021	5	O15733	O15733 dictyosteli
67	33	56.9	1063	4	Q8TDZ7	Q8tdz7 homo sapien
68	33	56.9	1235	16	Q929A9	Q929a9 listeria in
69	33	56.9	1235	16	Q8Y511	Q8y511 listeria mo
70	33	56.9	1824	5	Q9U0Y5	Q9u0y5 leishmania
71	32	55.2	61	10	Q8S6G8	Q8s6g8 oryza sativ
72	32	55.2	132	8	Q956K0	Q956k0 rhodotorula
73	32	55.2	136	16	Q8XFN0	Q8xfn0 salmonella
74	32	55.2	143	12	Q9WT48	Q9wt48 human herpe
75	32	55.2	143	12	Q9DYD9	Q9dyd9 human herpe

ALIGNMENTS

RESULT 1
Q55184
ID Q55184 PRELIMINARY; PRT; 333 AA.
AC Q55184;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein sll0456.
GN SLL0456.

```
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX   NCBI_TaxID=1148;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC 6803;
RA   Tabata S.;
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96127529; PubMed=8590279;
RA   Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA   Sugiura M., Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT   region from map positions 64% to 92% of the genome.";
RL   DNA Res. 2:153-166(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97061201; PubMed=8905231;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA   Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA   Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
DR   EMBL; D64001; BAA10324.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   333 AA;  37436 MW;  676E7399E4499ED6 CRC64;

  Query Match             70.7%;  Score 41;  DB 16;  Length 333;
  Best Local Similarity   77.8%;  Pred. No. 6.5;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              ||||||::|
Db        172 TVVYPTLVF 180


RESULT 2
O01574
ID   O01574      PRELIMINARY;      PRT;   974 AA.
AC   O01574;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 111.6 kDa protein.
GN   F48C1.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Gattung S., Le T.T.;
RT   "The sequence of C. elegans cosmid F48C1.";
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U97015; AAB52345.1; -.
DR   InterPro; IPR000602; Glyco_hydro_38.
DR   Pfam; PF01074; Glyco_hydro_38; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   974 AA;  111586 MW;  C825EFA33FB2F964 CRC64;

  Query Match             70.7%;  Score 41;  DB 5;  Length 974;
  Best Local Similarity   60.0%;  Pred. No. 18;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
                :|::|| |||
Db        851 QTIIYPPMMF 860


RESULT 3
Q9CIU3
ID   Q9CIU3      PRELIMINARY;      PRT;   394 AA.
AC   Q9CIU3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   ABC transporter ATP binding protein.
GN   YCGB OR LL0263.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC   Streptococcaceae; Lactococcus.
OX   NCBI_TaxID=1360;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
DR   EMBL; AE006263; AAK04361.1; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR001140; ABCtranprtrTM.
DR   InterPro; IPR003439; ABC_transportr.
DR   Pfam; PF00664; ABC_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transportr; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   394 AA;  43946 MW;  2822CBC28AEA4C36 CRC64;

  Query Match             65.5%;  Score 38;  DB 16;  Length 394;
  Best Local Similarity   66.7%;  Pred. No. 29;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |::|||| |
Db         47 TLIYPTMRF 55


RESULT 4
Q8VWX1
ID   Q8VWX1      PRELIMINARY;      PRT;   390 AA.
AC   Q8VWX1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Delta-15 desaturase.
GN   FAD3.
OS   Perilla frutescens.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
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OX   NCBI_TaxID=48386;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. OKDONG; TISSUE=DEVELOPING SEED;
RA   Kim K.-H., Hwang S.-K., Hwang Y.-S.;
RT   "Cloning of Perilla delta-15 desaturase.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF213482; AAL36934.1; -.
DR   InterPro; IPR001225; FA_desaturase.
DR   Pfam; PF00487; FA_desaturase; 1.
DR   ProDom; PD001081; FA_desaturase; 2.
SQ   SEQUENCE   390 AA;  44857 MW;  6959C941D47A15AB CRC64;

  Query Match             63.8%;  Score 37;  DB 10;  Length 390;
  Best Local Similarity   70.0%;  Pred. No. 44;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |:| | ||||
Db        241 TIVGPNMMFK 250


RESULT 5
Q9ZPP7
ID   Q9ZPP7      PRELIMINARY;      PRT;   391 AA.
AC   Q9ZPP7;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Omega-3 fatty acid desaturase.
GN   FAD3.
OS   Perilla frutescens.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
OX   NCBI_TaxID=48386;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. SUWON-8;
RX   MEDLINE=99205707; PubMed=10189709;
RA   Chung C.-H., Kim J.-L., Lee Y.-C., Choi Y.-L.;
RT   "Cloning and characterization of a seed-specific omega-3 fatty acid
RT   desaturase cDNA from Perilla frutescens.";
RL   Plant Cell Physiol. 40:114-118(1999).
DR   EMBL; AF047039; AAD15744.1; -.
DR   InterPro; IPR001225; FA_desaturase.
DR   Pfam; PF00487; FA_desaturase; 1.
DR   ProDom; PD001081; FA_desaturase; 2.
SQ   SEQUENCE   391 AA;  44931 MW;  6637E81654C17CEC CRC64;

  Query Match             63.8%;  Score 37;  DB 10;  Length 391;
  Best Local Similarity   70.0%;  Pred. No. 45;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |:| | ||||
Db        242 TIVGPNMMFK 251


RESULT 6
Q9I2X4
ID   Q9I2X4      PRELIMINARY;      PRT;   395 AA.
AC   Q9I2X4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Hypothetical protein PA1765.
GN   PA1765.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
DR   EMBL; AE004602; AAG05154.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   395 AA;  44670 MW;  FC183A433B2529C8 CRC64;

  Query Match             63.8%;  Score 37;  DB 16;  Length 395;
  Best Local Similarity   60.0%;  Pred. No. 45;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | ||||:::|
Db        292 RQVVYPSLLF 301


RESULT 7
Q9LUC5
ID   Q9LUC5      PRELIMINARY;      PRT;   512 AA.
AC   Q9LUC5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Cytochrome P450 (Putative cytochrome P450 protein).
GN   MIE1.20.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RA   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=20277480; PubMed=10819329;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT   features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT   clones.";
RL   DNA Res. 7:131-135(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA   Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA   Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA   Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA   Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA   Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA   Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA   Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT   "Full Length cDNA of gene MIE1.20 (GI:9294391).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR   EMBL; AB023038; BAB02401.1; -.
DR   EMBL; AY050827; AAK92762.1; -.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00385; P450.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   512 AA;  58442 MW;  19DDEEAD9C9BAF0B CRC64;
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  Query Match             62.1%;  Score 36;  DB 10;  Length 512;
  Best Local Similarity   63.6%;  Pred. No. 90;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | ||  |||
Db         80 RVVPYPLQMFK 90


RESULT 8
Q9FX69
ID   Q9FX69      PRELIMINARY;      PRT;   180 AA.
AC   Q9FX69;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   T6J4.4 protein.
GN   T6J4.4.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA   Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
RA   Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA   Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
RA   Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC011810; AAG09557.1; -.
SQ   SEQUENCE   180 AA;  19794 MW;  5DA0943DB333F332 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 180;
  Best Local Similarity   60.0%;  Pred. No. 51;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        124 RQLVYPTKLF 133


RESULT 9
Q93ZC5
ID   Q93ZC5      PRELIMINARY;      PRT;   254 AA.
AC   Q93ZC5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   At1g13280/T6J4_23.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA   Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA   Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA   Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA   Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA   Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA   Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA   Ecker J.R.;
RT   "Arabidopsis cDNA clones.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY057636; AAL15267.1; -.
SQ   SEQUENCE   254 AA;  27809 MW;  4D82FA4889242353 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 254;
  Best Local Similarity   60.0%;  Pred. No. 72;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        198 RQLVYPTKLF 207


RESULT 10
Q9LS01
ID   Q9LS01      PRELIMINARY;      PRT;   258 AA.
AC   Q9LS01;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Genomic DNA, chromosome 3, TAC clone:K13N2.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RA   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=20277480; PubMed=10819329;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT   features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT   clones.";
RL   DNA Res. 7:131-135(2000).
DR   EMBL; AB028607; BAA95765.1; -.
SQ   SEQUENCE   258 AA;  28398 MW;  42AF942E0E9AAB87 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 258;
  Best Local Similarity   60.0%;  Pred. No. 73;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        202 RQLVYPTKLF 211


RESULT 11
Q8ZLZ1
ID   Q8ZLZ1      PRELIMINARY;      PRT;   264 AA.
AC   Q8ZLZ1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative arylsulfate sulfotransferase.
GN   STM3192.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
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RL   Nature 413:852-856(2001).
DR   EMBL; AE008846; AAL22066.1; -.
KW   Transferase; Hypothetical protein; Complete proteome.
SQ   SEQUENCE   264 AA;  29462 MW;  2B3F39791813620F CRC64;

  Query Match             60.3%;  Score 35;  DB 16;  Length 264;
  Best Local Similarity   66.7%;  Pred. No. 74;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              :|:|| |||
Db        256 LVHPTQMFK 264


RESULT 12
Q94JV3
ID   Q94JV3      PRELIMINARY;      PRT;   282 AA.
AC   Q94JV3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   AT5g46920/MQD22_6.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA   Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA   Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA   Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
RA   Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA   Davis R.W., Theologis A., Ecker J.R.;
RT   "Arabidopsis cDNA clones.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF372919; AAK49635.1; -.
DR   InterPro; IPR000442; Intron_maturse2.
DR   Pfam; PF01348; Intron_maturas2; 1.
SQ   SEQUENCE   282 AA;  32875 MW;  89B0C6FFA2ABF4B8 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 282;
  Best Local Similarity   60.0%;  Pred. No. 79;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |||||: :
Db          9 RRVVYPTLRY 18


RESULT 13
Q8VGS2
ID   Q8VGS2      PRELIMINARY;      PRT;   320 AA.
AC   Q8VGS2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Olfactory receptor MOR187-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073074; AAL60737.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   320 AA;  36768 MW;  1FF2EBF1413280F1 CRC64;

  Query Match             60.3%;  Score 35;  DB 11;  Length 320;
  Best Local Similarity   75.0%;  Pred. No. 89;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMM 9
              ||:|| ||
Db         82 TVIYPKMM 89


RESULT 14
Q9WZI6
ID   Q9WZI6      PRELIMINARY;      PRT;   435 AA.
AC   Q9WZI6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PMBA-related protein.
GN   TM0727.
OS   Thermotoga maritima.
OC   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX   NCBI_TaxID=2336;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MSB8 / DSM 3109;
RX   MEDLINE=99287316; PubMed=10360571;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA   Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
DR   EMBL; AE001743; AAD35809.1; -.
DR   TIGR; TM0727; -.
DR   InterPro; IPR002510; PmbA_TldD.
DR   Pfam; PF01523; PmbA_TldD; 1.
KW   Complete proteome.
SQ   SEQUENCE   435 AA;  48306 MW;  C8764A342A975819 CRC64;

  Query Match             60.3%;  Score 35;  DB 16;  Length 435;
  Best Local Similarity   54.5%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | |: ||:|:|
Db        135 RVVMVPTVMYK 145


RESULT 15
Q9EME6
ID   Q9EME6      PRELIMINARY;      PRT;   504 AA.
AC   Q9EME6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   AMV260.
GN   AMV260.
OS   Amsacta moorei entomopoxvirus (AmEPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC   Entomopoxvirus B.
OX   NCBI_TaxID=28321;
RN   [1]
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RP   SEQUENCE FROM N.A.
RX   MEDLINE=20396580; PubMed=10936094;
RA   Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
RA   Moyer R.W.;
RT   "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
RT   Analysis and Comparison with Other Poxviruses.";
RL   Virology 274:120-139(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
RA   Moyer R.W.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF250284; AAG02966.1; -.
SQ   SEQUENCE   504 AA;  61862 MW;  ACA9BFFA559FAA50 CRC64;

  Query Match             60.3%;  Score 35;  DB 12;  Length 504;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              ||::|:::|:
Db        459 TVIFPSLLFR 468


RESULT 16
Q8Z3N6
ID   Q8Z3N6      PRELIMINARY;      PRT;   598 AA.
AC   Q8Z3N6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Probable arylsulfate sulfotransferase.
GN   STY3370.
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
DR   EMBL; AL627278; CAD07717.1; -.
KW   Transferase; Complete proteome.
SQ   SEQUENCE   598 AA;  66586 MW;  B5434F028A5421F0 CRC64;

  Query Match             60.3%;  Score 35;  DB 16;  Length 598;
  Best Local Similarity   66.7%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              :|:|| |||
Db        590 LVHPTQMFK 598


RESULT 17
Q8SWA5
ID   Q8SWA5      PRELIMINARY;      PRT;   705 AA.
AC   Q8SWA5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein ECU02_1230.
GN   ECU02_1230.
OS   Encephalitozoon cuniculi.
OC   Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX   NCBI_TaxID=6035;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GB-M1;
RA   Genoscope;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GB-M1;
RX   MEDLINE=21576510; PubMed=11719806;
RA   Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA   Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
RA   Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA   Weissenbach J., Vivares C.P.;
RT   "Genome sequence and gene compaction of the eukaryote parasite
RT   Encephalitozoon cuniculi.";
RL   Nature 414:450-453(2001).
DR   EMBL; AL590442; CAD25152.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   705 AA;  79649 MW;  235B834A40258AEF CRC64;

  Query Match             60.3%;  Score 35;  DB 5;  Length 705;
  Best Local Similarity   62.5%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMM 9
              ||:|||::
Db        570 TVIYPTLL 577


RESULT 18
Q8S7E2
ID   Q8S7E2      PRELIMINARY;      PRT;   733 AA.
AC   Q8S7E2;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 82.3 kDa protein.
GN   OSJNBA0057L21.15.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA   Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA   Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
RA   VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA   Salzberg S.L., White O., Fraser C.M.;
RT   "Oryza sativa chromosome 10 BAC OSJNBa0057L21 genomic sequence.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC087599; AAL79699.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   733 AA;  82297 MW;  24C8521E18220D9D CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 733;
  Best Local Similarity   60.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |||||: :
Db        462 RRVVYPTLRY 471


RESULT 19
Q9FJR9
ID   Q9FJR9      PRELIMINARY;      PRT;   735 AA.
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AC   Q9FJR9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Similarity to maturase-related protein.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=98403884; PubMed=9734815;
RA   Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA   Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT   Sequence features of the regions of 1,367,185 bp covered by 19
RT   physically assigned P1 and TAC clones.";
RL   DNA Res. 5:203-216(1998).
DR   EMBL; AB013394; BAB10231.1; -.
DR   InterPro; IPR000442; Intron_maturse2.
DR   InterPro; IPR000477; RVTse.
DR   Pfam;.PF01348; Intron_maturas2; 1.
DR   Pfam; PF00078; rvt; 1.
KW   RNA-directed DNA polymerase.
SQ   SEQUENCE   735 AA;  85179 MW;  3C4A940CDA6E1590 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 735;
  Best Local Similarity   60.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |||||: :
Db        462 RRVVYPTLRY 471


RESULT 20
Q9ZVV2
ID   Q9ZVV2      PRELIMINARY;      PRT;   887 AA.
AC   Q9ZVV2;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   T5A14.3 protein.
GN   T5A14.3.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA   Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA   Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA   Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC005223; AAD10640.1; -.
DR   HSSP; P17119; 3KAR.
DR   InterPro; IPR001752; kinesin_motor.
DR   Pfam; PF00225; kinesin; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW   ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ   SEQUENCE   887 AA;  99904 MW;  748B215B02E2E9BC CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 887;
  Best Local Similarity   70.0%;  Pred. No. 2.4e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              ||| ||:| |
Db        696 TVVNPTLMLK 705


RESULT 21
Q9HFQ9
ID   Q9HFQ9      PRELIMINARY;      PRT;  1030 AA.
AC   Q9HFQ9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chitinase.
GN   CHIC.
OS   Emericella nidulans (Aspergillus nidulans).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=5072;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FGSC 4;
RA   Specht C.A., Benfield B.B., Garcia J.J.;
RT   "Identification of bacteria-like chitinases in fungi.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF314225; AAG34171.1; -.
DR   HSSP; P10968; 2CWG.
DR   InterPro; IPR001579; Chitinase_18/2.
DR   InterPro; IPR001002; Chitin_binding_1.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   Pfam; PF00187; Chitin_bind_1; 1.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   ProDom; PD000471; Glyco_hydro_18; 1.
DR   ProDom; PD000609; Chitin_binding_1; 1.
DR   SMART; SM00270; ChtBD1; 2.
DR   PROSITE; PS01095; CHITINASE_18; 1.
DR   PROSITE; PS00026; CHITIN_BINDING; 1.
KW   Chitin-binding.
SQ   SEQUENCE   1030 AA;  112748 MW;  8EE1E64192AF03E5 CRC64;

  Query Match             60.3%;  Score 35;  DB 3;  Length 1030;
  Best Local Similarity   66.7%;  Pred. No. 2.7e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              || |||: |
Db        951 TVTYPTLTF 959


RESULT 22
Q84121
ID   Q84121      PRELIMINARY;      PRT;    54 AA.
AC   Q84121;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Influenza A/Shearwater/Australia/75 (H5N3), neuraminidase (Seg 6), 5'
DE   end (Fragment).
OS   Influenzavirus A.
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenza A viruses.
OX   NCBI_TaxID=11320;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83017869; PubMed=6927853;
RA   Blok J., Air G.M.;
RT   "Sequence variation at the 3' end of the neuraminidase gene from 39
RT   influenza type A viruses.";
RL   Virology 121:211-229(1982).
DR   EMBL; K01014; AAA43416.1; -.
DR   InterPro; IPR001860; GH_34.
DR   Pfam; PF00064; neur; 1.
FT   NON_TER      54      54
SQ   SEQUENCE   54 AA;  5916 MW;  B0BD49BBF05D0153 CRC64;
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RESULT 23
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AC   Q8UUZ6;
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DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Alpha A crystallin.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LENS;
RA   Runkle S., Hill J., Kantorow M., Horwitz J., Posner M.;
RT   "Cloning and characterization of zebrafish (Danio rerio) alpha A-
RT   crystallin.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY035778; AAK61363.1; -.
DR   InterPro; IPR001436; Crystallin_alpha.
DR   InterPro; IPR003090; Crystallin_N.
DR   InterPro; IPR002068; Hsp20.
DR   Pfam; PF00525; crystallin; 1.
DR   Pfam; PF00011; HSP20; 1.
DR   PRINTS; PR00299; ACRYSTALLIN.
DR   ProDom; PD001193; Crystallin_N; 1.
DR   PROSITE; PS01031; HSP20; 1.
SQ   SEQUENCE   173 AA;  19714 MW;  301D743DB91BBC13 CRC64;

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Db         12 RTLGYPTRLF 21


RESULT 24
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ID   Q98ID0      PRELIMINARY;      PRT;   180 AA.
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DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein mll2459.
GN   MLL2459.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
DR   EMBL; AP002999; BAB49586.1; -.
DR   InterPro; IPR005149; PadR.
DR   Pfam; PF03551; PadR; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   180 AA;  19909 MW;  D94F736B2855CF60 CRC64;

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Db         49 VVYPTLTF 56


RESULT 25
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DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein CPE0414.
GN   CPE0414.
OS   Clostridium perfringens.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC   Clostridiales; Clostridiaceae; Clostridium.
OX   NCBI_TaxID=1502;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=13 / TYPE A;
RX   PubMed=11792842;
RA   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA   Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT   "Complete genome sequence of Clostridium perfringens, an anaerobic
RT   flesh-eater.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR   EMBL; AP003186; BAB80120.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   212 AA;  24363 MW;  DB7E1E2AC94BE697 CRC64;

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Qy          4 VYPTMMFK 11
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Db        205 IYPNMIFK 212


Search completed: July 16, 2003, 14:37:07
Job time : 42 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 44.3333 Seconds
(without alignments)
33.062 Million cell updates/sec

Title: US-09-923-716C-4
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	65.5	207	21	AAG29277	Arabidopsis thalia
2	38	65.5	262	18	AAW27262	Plant steroid 5-al
3	38	65.5	262	21	AAG29276	Arabidopsis thalia
4	38	65.5	394	23	ABB53569	Lactococcus lactis
5	37	63.8	560	22	ABG29423	Novel human diagno
6	36	62.1	82	22	AAO10186	Human polypeptide
7	35	60.3	242	21	AAG09307	Arabidopsis thalia
8	35	60.3	244	21	AAG07361	Arabidopsis thalia
9	35	60.3	244	21	AAG61263	Arabidopsis thalia
10	35	60.3	246	21	AAY32315	Soybean neutral tr
11	35	60.3	251	21	AAG07360	Arabidopsis thalia
12	35	60.3	251	21	AAG61262	Arabidopsis thalia
13	35	60.3	252	21	AAG09306	Arabidopsis thalia
14	35	60.3	254	21	AAG09305	Arabidopsis thalia
15	35	60.3	254	22	AAB86353	A. thaliana allene
16	35	60.3	254	23	ABB90980	Herbicidally activ
17	35	60.3	258	21	AAG07359	Arabidopsis thalia
18	35	60.3	258	21	AAG61261	Arabidopsis thalia
19	34	58.6	56	21	AAG55171	Arabidopsis thalia
20	34	58.6	56	21	AAG60760	Arabidopsis thalia
21	34	58.6	57	21	AAG55170	Arabidopsis thalia
22	34	58.6	57	21	AAG60759	Arabidopsis thalia
23	34	58.6	264	21	AAG05880	Arabidopsis thalia
24	34	58.6	264	21	AAG51213	Arabidopsis thalia
25	34	58.6	264	22	AAM78329	Human protein SEQ
26	34	58.6	266	21	AAG51212	Arabidopsis thalia
27	34	58.6	267	21	AAG05879	Arabidopsis thalia
28	34	58.6	322	20	AAY30161	Human dorsal root
29	34	58.6	322	20	AAY30162	Human dorsal root
30	34	58.6	322	22	AAE12794	Human G protein co
31	34	58.6	322	22	AAU04371	Human G-protein co
32	34	58.6	322	22	AAG64294	Human GTP-binding
33	34	58.6	322	23	AAE21288	Human MrgX1 (mas-r
34	34	58.6	322	23	AAE17074	Human G-protein co
35	34	58.6	591	21	AAY58905	Rhinocladiella atr
36	34	58.6	598	21	AAY58903	Rhinocladiella atr
37	33.5	57.8	1810	22	ABB71194	Drosophila melanog
38	33	56.9	99	23	ABP41643	Human ovarian anti
39	33	56.9	310	21	AAB21021	Human nucleic acid
40	33	56.9	593	22	AAU51414	Propionibacterium
41	33	56.9	609	20	AAW82726	Adenovirus pACTSsi
42	33	56.9	609	20	AAW82727	Adenovirus Pig4KN
43	33	56.9	656	22	AAG90823	C glutamicum prote
44	33	56.9	700	22	AAB28610	Yeast RF1. Uniden
45	33	56.9	725	22	ABB68684	Drosophila melanog
46	33	56.9	750	20	AAW82728	Adenovirus PNSPig4
47	33	56.9	1235	23	ABB48680	Listeria monocytog
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49	32	55.2	72	23	ABP33743	Human ORF2716 prot
50	32	55.2	74	23	AAO21674	Human secreted pro
51	32	55.2	93	22	AAM83247	Human immune/haema
52	32	55.2	137	22	AAU45923	Propionibacterium
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54	32	55.2	283	23	ABB49253	Listeria monocytog
55	32	55.2	358	23	AAM52346	Hydratase-aldorase
56	32	55.2	446	20	AAY42113	Corn anthranilate
57	32	55.2	447	22	AAU03135	Streptococcus pyog
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59	32	55.2	447	23	ABP30002	Streptococcus poly
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62	32	55.2	462	21	AAY68843	Amino acid sequenc
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66	32	55.2	487	21	AAY58912	Amino polyol amine
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68	32	55.2	491	20	AAY41302	Tobacco anthranila
69	32	55.2	519	23	ABP27100	Streptococcus poly
70	32	55.2	526	23	ABB92684	Herbicidally activ
71	32	55.2	554	21	AAY58910	Amino polyol amine
72	32	55.2	554	21	AAY68846	An aminopolyol ami
73	32	55.2	577	20	AAW93815	Rice ASA first iso
74	32	55.2	577	20	AAW93810	Rice anthranilate
75	32	55.2	595	23	ABB93363	Herbicidally activ

ALIGNMENTS

RESULT 1
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ID AAG29277 standard; Protein; 207 AA.

XX
AC AAG29277;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34806.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
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XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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  Best Local Similarity   45.5%;  Pred. No. 9.2;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
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Db         38 RTIIYPLRLFR 48


RESULT 2
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ID   AAW27262 standard; Protein; 262 AA.
XX
AC   AAW27262;
XX
DT   23-APR-1998  (first entry)
XX
DE   Plant steroid 5-alpha reductase DET2.
XX
KW   Plant steroid 5-alpha reductase; Arabidopsis; DET2; pest resistance;
KW   brassinolide biosynthesis; growth.
XX
OS   Arabidopsis sp.
XX
PN   WO9739112-A1.
XX
PD   23-OCT-1997.
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PF   14-APR-1997;   97WO-US06115.
XX
PR   18-APR-1996;   96US-0634475.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Chory J,  Li J;
XX
DR   WPI; 1997-526449/48.
DR   N-PSDB; AAT91260.
XX
PT   New isolated plant steroid 5-alpha reductase gene, DET2 - used to
PT   develop products for e.g. increasing plant yield and pest resistance
PT   or for producing plants with reduced stature
XX
PS   Claim 4; Page 45-46; 70pp; English.
XX
CC   The present sequence represents a novel plant steroid 5-alpha reductase,
CC   DET2. Methods have also been developed for producing plants with
CC   increased yield, as compared to wild-type. The DET2 polypeptides have
CC   5AR activity and are involved in the brassinolide biosynthesis pathway.
CC   The products and methods can be used to produce modified plants which
CC   can exhibit increased plant growth, increased crop yield or increased
CC   biomass. The plants can also have increased resistance to pests and
CC   pesticides. Inhibitors of DET2 can be used to cause loss of function of
CC   DET2 resulting in, e.g. male sterile plants or reduced stature (dwarf
CC   plants).
XX
SQ   Sequence   262 AA;

  Query Match             65.5%;  Score 38;  DB 18;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 12;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 3
AAG29276
ID   AAG29276 standard; Protein; 262 AA.
XX
AC   AAG29276;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 34805.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
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PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
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PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
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PR 01-JUN-1999; 99US-0137222.
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PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
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PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
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PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
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PR 20-AUG-1999; 99US-0149722.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.

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PR   07-OCT-1999;   99US-0158029.
PR   08-OCT-1999;   99US-0158232.
PR   12-OCT-1999;   99US-0158369.
PR   13-OCT-1999;   99US-0159293.
PR   13-OCT-1999;   99US-0159294.
PR   13-OCT-1999;   99US-0159295.
PR   14-OCT-1999;   99US-0159329.
PR   14-OCT-1999;   99US-0159330.
PR   14-OCT-1999;   99US-0159331.
PR   14-OCT-1999;   99US-0159637.
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PR   18-OCT-1999;   99US-0159584.
PR   21-OCT-1999;   99US-0160741.
PR   21-OCT-1999;   99US-0160767.
PR   21-OCT-1999;   99US-0160768.
PR   21-OCT-1999;   99US-0160770.
PR   21-OCT-1999;   99US-0160814.
PR   21-OCT-1999;   99US-0160815.
PR   22-OCT-1999;   99US-0160980.
PR   22-OCT-1999;   99US-0160981.
PR   22-OCT-1999;   99US-0160989.
PR   25-OCT-1999;   99US-0161404.
PR   25-OCT-1999;   99US-0161405.
PR   25-OCT-1999;   99US-0161406.
PR   26-OCT-1999;   99US-0161359.
PR   26-OCT-1999;   99US-0161360.
PR   26-OCT-1999;   99US-0161361.
PR   28-OCT-1999;   99US-0161920.
PR   28-OCT-1999;   99US-0161992.
PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

  Query Match             65.5%;  Score 38;  DB 21;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 12;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 4
ABB53569
ID   ABB53569 standard; Protein; 394 AA.
XX
AC   ABB53569;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Lactococcus lactis protein ycgB.
XX
KW   Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX
OS   Lactococcus lactis IL1403.
XX
PN   FR2807446-A1.
XX
PD   12-OCT-2001.
XX
PF   11-APR-2000; 2000FR-0004630.
XX
PR   11-APR-2000; 2000FR-0004630.
XX
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
PI   Bolotine A,  Sorokine A,  Renault P,  Ehrlich SD;
XX
DR   WPI; 2002-043418/06.
XX
PT   New nucleotide sequence useful in the identification or Lactococcus
PT   lactis and related species -
XX
PS   Claim 6; SEQ ID No 271; 2504pp; French.
XX
CC   The present invention is related to a Lactococcus lactis nucleotide
CC   sequence (ABA90521) and related proteins (ABB53300-ABB55621). The
CC   nucleic acid sequence is useful in the detection and/or amplification of
CC   nucleic acid sequence, particularly to identify Lactococcus lactis or
CC   related species. The proteins of the invention are useful for the
CC   biosynthesis or biodegradation of a composition of interest. The
CC   invention helps research in lactic bacteria, particularly useful in the
CC   production of yogurt and cheese.
CC   Note: The sequence data for this patent is based on equivalent patent
CC   WO200177334 (published 18-OCT-2001) which is available in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   394 AA;

  Query Match             65.5%;  Score 38;  DB 23;  Length 394;
  Best Local Similarity   66.7%;  Pred. No. 19;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |::|||| |
Db         47 TLIYPTMRF 55


RESULT 5
ABG29423
ID   ABG29423 standard; Protein; 560 AA.
XX
AC   ABG29423;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #29414.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS93610.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 59782; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
```

CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 560 AA;

Query Match 63.8%; Score 37; DB 22; Length 560;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TVVYPTMMF 10
|:| |||||
Db 214 TLVIPTMMF 222

RESULT 6
AAO10186
ID AAO10186 standard; Protein; 82 AA.
XX
AC AAO10186;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 24078.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI90117.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 24078; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 82 AA;

Query Match 62.1%; Score 36; DB 22; Length 82;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YPTMMFK 11
||||:||
Db 1 YPTMIFK 7

RESULT 7
AAG09307
ID AAG09307 standard; Protein; 242 AA.
XX
AC AAG09307;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7187.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
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PR 18-JUN-1999; 99US-0139457.
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PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
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PR 23-JUN-1999; 99US-0140354.
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PR 28-JUN-1999; 99US-0140823.
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PR 02-JUL-1999; 99US-0142055.
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PR 08-JUL-1999; 99US-0142803.
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PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
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PR 21-JUL-1999; 99US-0144814.
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PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
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Query Match 60.3%; Score 35; DB 21; Length 242;
Best Local Similarity 60.0%; Pred. No. 45;

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Db        186 RQLVYPTKLF 195


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KW   hybridisation assay; genetic mapping; gene expression control; promoter;
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Query Match 60.3%; Score 35; DB 21; Length 244;
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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Query Match 60.3%; Score 35; DB 21; Length 244;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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KW vegetable oil; transgenic plant.
XX
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XX
PD 04-NOV-1999.
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XX
DR WPI; 2000-062036/05.
DR N-PSDB; AAZ34964.
XX
PT Novel plant triacylglycerol lipase polynucleotides used to alter the
PT level of the enzyme in transgenic plants -
XX
PS Claim 10; Page 58-59; 65pp; English.
XX
CC This sequence represents most of a soybean neutral triacylglycerol
CC lipase (TAGL), as deduced from the nucleotide sequence of isolated
CC cDNA clones (see AAZ34964). Novel acid and neutral TAGL polypeptides
CC (see AAY32301-17) and polynucleotides (see AAZ34950-66) from corn,
CC Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes
CC may be prepared recombinantly and used to raise antibodies, which
CC are used for detecting the enzymes in situ in cells or in vitro in
CC cell extracts. The polynucleotides may be used to create transgenic
CC plants in which the TAGL levels are present at higher or lower levels
CC than normal, or in cell types or developmental processes where they are
CC not normally found. This would alter the level of triacylglycerol and
CC cholesteryl esters found in those cells. Accumulation of fatty acids
CC with unusual structures may be a positive phenotype in plants used for
CC foods. In addition, it may be desirable to eliminate expression of TAGL
CC genes for certain applications. TAGL enzymes may also be useful for the
CC processing of plant seed oils and for the development of novel seed
CC oils. The TAGL enzymes can also be used as targets to facilitate the
CC design and/or identification of inhibitors of those enzymes that may be
CC useful as herbicides. This is desirable because inhibition of the
CC activity of either of the enzymes could lead to an inhibition of plant
CC growth.
XX
SQ Sequence 246 AA;

Query Match 60.3%; Score 35; DB 21; Length 246;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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Best Local Similarity 60.0%; Pred. No. 47;
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DT 18-OCT-2000 (first entry)
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
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PD 06-SEP-2000.

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KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
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PR 16-JUL-1999; 99US-0144086.
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PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151066.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 35; DB 21; Length 252;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RTVVYPTMMF 10
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Db        196 RQLVYPTKLF 205
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RESULT 14
AAG09305
ID AAG09305 standard; Protein; 254 AA.
XX
AC AAG09305;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7185.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 29-MAR-1999; 99US-0126785.
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PR 19-APR-1999; 99US-0130077.

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PR 08-OCT-1999; 99US-0158232.
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Query Match 60.3%; Score 35; DB 21; Length 254;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
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Db 198 RQLVYPTKLF 207

RESULT 15
AAB86353
ID AAB86353 standard; Protein; 254 AA.
XX
AC AAB86353;
XX
DT 20-SEP-2001 (first entry)
XX
DE A. thaliana allene oxide cyclase protein SEQ ID 10.
XX
KW Allene oxide cyclase; jasmonic acid; plant; AOC; jasmonate biosynthesis;
KW signalling molecule; gene expression; stress response; perfume synthesis;
KW wound-induced signal cascade; defensive response; transgenic plant;
KW protease inhibitor synthesis; phytoalexin synthesis; alkaloid synthesis;
KW pathogen resistance; herbicide resistance; ultra-violet protection;
KW secondary metabolite production; male sterility; flower development;
KW seed formation; germination.
XX
OS Arabidopsis thaliana.
XX
PN WO200157224-A2.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-EP01148.
XX
PR 02-FEB-2000; 2000DE-1004468.
XX
PA (PFLA-) INST PFLANZENBIOCHEMIE.
XX
PI Ziegler J, Stenzel I, Hause B, Wasternack C;
XX
DR WPI; 2001-483438/52.
DR N-PSDB; AAH21490.
XX
PT Nucleic acid encoding plant allene oxide cyclase, useful for producing
PT transgenic plants with altered jasmonic acid synthesis, e.g. increased
PT resistance to pathogens -
XX
PS Claim 1b; Page 55-56; 66pp; German.
XX
CC This invention describes novel nucleic acids (I), encoding proteins
CC (II) with the activity of the allene oxide cyclase (AOC) involved in
CC jasmonate biosynthesis. Jasmonic acid (JA) is a signalling molecule
CC involved in: (i) altered gene expression in plants in response to
CC stress; and (ii) developmental processes. It is also an intermediate in
CC the wound-induced signal cascade and induces many defensive responses in
CC plants, including synthesis of protease inhibitors, phytoalexins,
CC alkaloids and perfumes. (I) is used: (i) to produce transgenic plants,
CC cells etc. with altered AOC activity, specifically altered resistance to
CC pathogens and herbivores, optimal plant/useful insect/pest interaction;
CC increased biomass, altered carbohydrate and nitrogen metabolism;
CC increased production of secondary metabolites (especially alkaloids
CC and/or phytoalexins), optimal ultra-violet protection; altered male
CC sterility and/or altered development, especially flower development, seed
CC formation and/or germination; (ii) for selective production of 9S/13S
CC (cis(+))-12-oxophytodienoic acid (III), a precursor of jasmonic acid
CC (JA); (iii) for isolation of homologous sequences; and (iv) to express
CC AOC in prokaryotic or eukaryotic cells or (in antisense orientation) to
CC inhibit its expression. (I) Makes possible large scale production of high
CC purity JA. (I) is very specific for production of (III) (contrast
CC non-enzymatic methods which produce mixtures of isomers) which is a
CC precursor for the natural enantiomer of JA. This sequence represents the
CC Arabidopsis thaliana AOC described in the invention.
XX
SQ Sequence 254 AA;

Query Match 60.3%; Score 35; DB 22; Length 254;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
| :|||| :|
Db 198 RQLVYPTKLF 207

RESULT 16
ABB90980
ID ABB90980 standard; Protein; 254 AA.
XX
AC ABB90980;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 191.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP09892.
XX
PR 28-AUG-2001; 2001WO-EP09892.
XX
PA (FARB) BAYER AG.
XX
PI Tietjen K, Weidler M;
XX
DR WPI; 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
XX
PS Claim 5; SEQ ID NO 191; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising

CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX
SQ Sequence 254 AA;

Query Match 60.3%; Score 35; DB 23; Length 254;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTVVYPTMMF 10
| :|||| :|
Db 198 RQLVYPTKLF 207

RESULT 17
AAG07359
ID AAG07359 standard; Protein; 258 AA.
XX
AC AAG07359;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4483.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
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PR 07-MAY-1999; 99US-0132863.
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PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
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PN   EP1033405-A2.
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PD   06-SEP-2000.
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Query Match 58.6%; Score 34; DB 21; Length 56;
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
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Query Match 58.6%; Score 34; DB 21; Length 56;
Best Local Similarity 45.5%; Pred. No. 14;
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
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Query Match 58.6%; Score 34; DB 21; Length 57;
Best Local Similarity 45.5%; Pred. No. 14;
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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XX

PN EP1033405-A2.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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XX
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
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PR 29-OCT-1999; 99US-0162142.

Query Match 58.6%; Score 34; DB 21; Length 264;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db        106 VVYPAVMF 113
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DT 06-NOV-2001 (first entry)
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DE Human protein SEQ ID NO 991.
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KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
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PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK51462.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3215-3216; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 264 AA;

Query Match 58.6%; Score 34; DB 22; Length 264;
Best Local Similarity 62.5%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db         97 ILYPVMMF 104
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Job time : 45.3333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2003, 14:31:07 ; Search time 15 Seconds
(without alignments)
21.577 Million cell updates/sec

Title: US-09-923-716C-4
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Sequence: 1 RTVVYPTMMFK 11

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Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	38	65.5	246	4	US-09-709-791-3	Sequence 3, Appli
3	38	65.5	262	4	US-08-634-475-2	Sequence 2, Appli
4	38	65.5	262	4	US-09-709-791-2	Sequence 2, Appli
5	34	58.6	591	4	US-09-352-159-46	Sequence 46, Appl
6	34	58.6	598	4	US-09-352-159-42	Sequence 42, Appl
7	33	56.9	700	4	US-08-274-121B-5	Sequence 5, Appli
8	32	55.2	462	4	US-09-352-159-6	Sequence 6, Appli
9	32	55.2	462	4	US-09-352-159-8	Sequence 8, Appli
10	32	55.2	462	4	US-09-352-168-6	Sequence 6, Appli
11	32	55.2	462	4	US-09-352-168-8	Sequence 8, Appli
12	32	55.2	463	4	US-09-352-159-11	Sequence 11, Appl
13	32	55.2	463	4	US-09-352-168-11	Sequence 11, Appl
14	32	55.2	468	2	US-08-959-011-3	Sequence 3, Appli
15	32	55.2	487	4	US-09-352-159-21	Sequence 21, Appl
16	32	55.2	487	4	US-09-352-168-21	Sequence 21, Appl
17	32	55.2	491	2	US-09-001-826-23	Sequence 23, Appl
18	32	55.2	554	4	US-09-352-159-17	Sequence 17, Appl
19	32	55.2	554	4	US-09-352-168-17	Sequence 17, Appl
20	32	55.2	577	4	US-09-486-382B-2	Sequence 2, Appli
21	32	55.2	577	4	US-09-486-382B-13	Sequence 13, Appl
22	32	55.2	595	3	US-08-604-789B-3	Sequence 3, Appli
23	32	55.2	595	4	US-09-312-721A-3	Sequence 3, Appli
24	32	55.2	598	4	US-09-352-159-40	Sequence 40, Appl
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27	32	55.2	600	4	US-09-352-159-38	Sequence 38, Appl
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29	32	55.2	692	4	US-09-352-159-19	Sequence 19, Appl
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33	32	55.2	991	4	US-09-352-159-27	Sequence 27, Appl
34	32	55.2	991	4	US-09-352-168-27	Sequence 27, Appl
35	32	55.2	1000	4	US-09-352-159-25	Sequence 25, Appl
36	32	55.2	1000	4	US-09-352-168-25	Sequence 25, Appl
37	32	55.2	1196	4	US-09-352-159-31	Sequence 31, Appl
38	32	55.2	1196	4	US-09-352-168-31	Sequence 31, Appl
39	32	55.2	1205	4	US-09-352-159-29	Sequence 29, Appl
40	32	55.2	1205	4	US-09-352-168-29	Sequence 29, Appl
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42	31	53.4	149	4	US-09-134-001C-2957	Sequence 2957, Ap
43	31	53.4	201	2	US-08-933-750C-21	Sequence 21, Appl
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45	31	53.4	320	2	US-08-933-750C-12	Sequence 12, Appl
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51	31	53.4	1487	4	US-09-185-373-4	Sequence 4, Appli
52	31	53.4	3011	3	US-08-811-566-20	Sequence 20, Appl
53	31	53.4	3011	4	US-09-014-416-1	Sequence 1, Appli
54	31	53.4	3011	4	US-09-014-416-5	Sequence 5, Appli
55	31	53.4	3011	4	US-09-034-756-20	Sequence 20, Appl
56	31	53.4	3012	3	US-08-811-566-2	Sequence 2, Appli
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58	30.5	52.6	371	4	US-09-574-141A-56	Sequence 56, Appl
59	30	51.7	280	6	5182210-12	Patent No. 5182210
60	30	51.7	451	1	US-08-625-322-4	Sequence 4, Appli
61	30	51.7	490	2	US-08-673-789-13	Sequence 13, Appl
62	30	51.7	621	3	US-08-604-789B-4	Sequence 4, Appli
63	30	51.7	621	4	US-09-312-721A-4	Sequence 4, Appli
64	30	51.7	697	2	US-08-674-351-4	Sequence 4, Appli
65	30	51.7	701	4	US-09-132-028-2	Sequence 2, Appli
66	30	51.7	722	4	US-09-134-001C-5482	Sequence 5482, Ap
67	30	51.7	744	1	US-08-162-809-20	Sequence 20, Appl
68	30	51.7	1437	3	US-09-061-400-2	Sequence 2, Appli
69	30	51.7	1453	2	US-09-001-273-2	Sequence 2, Appli
70	30	51.7	1453	4	US-08-843-459A-2	Sequence 2, Appli
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72	29	50.0	68	4	US-09-097-889-17	Sequence 17, Appl
73	29	50.0	156	4	US-09-134-001C-4450	Sequence 4450, Ap
74	29	50.0	305	4	US-08-858-207A-392	Sequence 392, App
75	29	50.0	401	4	US-09-134-001C-4403	Sequence 4403, Ap

ALIGNMENTS

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; Patent No. 6143950
;  GENERAL INFORMATION:
;    APPLICANT:  Chory et al., Joanne
;    TITLE OF INVENTION:  NOVEL PLANT STEROID 5 alpha REDUCTASE,
;    TITLE OF INVENTION:  DET2
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/634,475
;      FILING DATE:  18-APR-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07251/015001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-634-475-3

  Query Match             65.5%;  Score 38;  DB 4;  Length 246;
  Best Local Similarity   45.5%;  Pred. No. 8.3;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

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Db         77 RTIIYPLRLFR 87


RESULT 2
US-09-709-791-3
; Sequence 3, Application US/09709791
; Patent No. 6352846
;   GENERAL INFORMATION:
;        APPLICANT: Chory, Joanne
;                   Li, Jianming
;        TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
;                            DET2
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
;             STREET: 620 Newport Center Drive, 16th floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/709,791
;             FILING DATE: 07-No. 6352846-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fuller, Michael
;             REGISTRATION NUMBER: 36,516
;             REFERENCE/DOCKET NUMBER: SALKINS.010DV1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/235-8550
;             TELEFAX: 619/235-0176
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 246 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: not relevant
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-709-791-3

  Query Match             65.5%;  Score 38;  DB 4;  Length 246;
  Best Local Similarity   45.5%;  Pred. No. 8.3;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

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Db         77 RTIIYPLRLFR 87


RESULT 3
US-08-634-475-2
; Sequence 2, Application US/08634475
; Patent No. 6143950
;  GENERAL INFORMATION:
;    APPLICANT:  Chory et al., Joanne
;    TITLE OF INVENTION:  NOVEL PLANT STEROID 5 alpha REDUCTASE,
;    TITLE OF INVENTION:  DET2
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/634,475
;      FILING DATE:  18-APR-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07251/015001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  262 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-634-475-2

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Db         93 RTIIYPLRLFR 103


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; Sequence 2, Application US/09709791
; Patent No. 6352846
;   GENERAL INFORMATION:
;        APPLICANT: Chory, Joanne
;                   Li, Jianming
;        TITLE OF INVENTION: NOVEL PLANT STEROID 5 alpha REDUCTASE,
;                            DET2
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
;             STREET: 620 Newport Center Drive, 16th floor
;             CITY: Newport Beach
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;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/709,791
;             FILING DATE: 07-No. 6352846-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fuller, Michael
;             REGISTRATION NUMBER: 36,516
;             REFERENCE/DOCKET NUMBER: SALKINS.010DV1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/235-8550
;             TELEFAX: 619/235-0176
;    INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 262 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: not relevant
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-709-791-2

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RESULT 5
US-09-352-159-46
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; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 46
;   LENGTH: 591
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
US-09-352-159-46

  Query Match             58.6%;  Score 34;  DB 4;  Length 591;
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  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        405 TTLYPTLIF 413


RESULT 6
US-09-352-159-42
; Sequence 42, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 42
;   LENGTH: 598
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
US-09-352-159-42

  Query Match             58.6%;  Score 34;  DB 4;  Length 598;
  Best Local Similarity   55.6%;  Pred. No. 1.1e+02;
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Db        406 TTLYPTLIF 414


RESULT 7
US-08-274-121B-5
; Sequence 5, Application US/08274121B
; Patent No. 6133034
;  GENERAL INFORMATION:
;    APPLICANT:  Arne Reidar Strom
;    APPLICANT:  Inga Kaasen
;    APPLICANT:  Olaf Bay Styrvold
;    APPLICANT:  John McDougall
;    TITLE OF INVENTION:  Methods and Compositions
;    TITLE OF INVENTION:  Related To The Production
;    TITLE OF INVENTION:  of Trehalose
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calgene, Inc.
;      STREET:  1920 Fifth Street
;      CITY:  Davis
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  95616
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 2.0 MB
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.1(a)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/274,121B
;      FILING DATE:  12-JULY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/893,099
;      FILING DATE:  27-MAY-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elizabeth Lassen
;      REGISTRATION NUMBER:  31,845
;      NAME:  Donna E. Scherer
;      REGISTRATION NUMBER:  34,719
;      REFERENCE/DOCKET NUMBER:  CGNE 86(1)
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (916) 753-6313
;      TELEFAX:  (916) 753-1510
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  700 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-274-121B-5

  Query Match             56.9%;  Score 33;  DB 4;  Length 700;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              : ::|||  |
Db        672 KAIIYPTFFF 681


RESULT 8
US-09-352-159-6
; Sequence 6, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-6

  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 9
US-09-352-159-8
; Sequence 8, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-8

  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 10
US-09-352-168-6
; Sequence 6, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-168-6

  Query Match             55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 11
US-09-352-168-8
; Sequence 8, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-168-8
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```
  Query Match           55.2%;  Score 32;  DB 4;  Length 462;
  Best Local Similarity  55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 12
US-09-352-159-11
; Sequence 11, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-11

  Query Match           55.2%;  Score 32;  DB 4;  Length 463;
  Best Local Similarity  55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 13
US-09-352-168-11
; Sequence 11, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   OTHER INFORMATION: Extra lysine in the polypeptide sequence of
;   OTHER INFORMATION: K:trAPAO, 463 aa.
US-09-352-168-11

  Query Match           55.2%;  Score 32;  DB 4;  Length 463;
  Best Local Similarity  55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 14
US-08-959-011-3
; Sequence 3, Application US/08959011
; Patent No. 5932444
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  VACUOLAR ATPASE SUBUNIT AC45
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,011
;      FILING DATE:  Herewith
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0412 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  497984
US-08-959-011-3

  Query Match           55.2%;  Score 32;  DB 2;  Length 468;
  Best Local Similarity  87.5%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTM 8
              |||| |||
Db        244 RTVVPPTM 251


RESULT 15
US-09-352-159-21
; Sequence 21, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
```

```
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;    LENGTH: 487
;    TYPE: PRT
;    ORGANISM: Unknown
;    FEATURE:
;    NAME/KEY: SIGNAL
;    LOCATION: (1)...(24)
US-09-352-159-21

  Query Match             55.2%;  Score 32;  DB 4;  Length 487;
  Best Local Similarity   55.6%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        295 TTLYPTLTF 303


RESULT 16
US-09-352-168-21
; Sequence 21, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;    LENGTH: 487
;    TYPE: PRT
;    ORGANISM: Unknown
;    FEATURE:
;    NAME/KEY: SIGNAL
;    LOCATION: (1)...(24)
;    OTHER INFORMATION: K:trAPAO translational fusion with barley alpha
;    OTHER INFORMATION: amylase signal sequence, for expression and
;    OTHER INFORMATION: secretion of the mature trAPAO in maize.
US-09-352-168-21

  Query Match             55.2%;  Score 32;  DB 4;  Length 487;
  Best Local Similarity   55.6%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        295 TTLYPTLTF 303


RESULT 17
US-09-001-826-23
; Sequence 23, Application US/09001826A
; Patent No. 5965727
; GENERAL INFORMATION:
;  APPLICANT: SONG, HEE-SOOK
;  APPLICANT: BROTHERTON, JEFFREY E.
;  APPLICANT: WIDHOLM, JACK M.
;  TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
;  TITLE OF INVENTION: TRANSFORMATION
;  FILE REFERENCE: UI001.C1
;  CURRENT APPLICATION NUMBER: US/09/001,826A
;  CURRENT FILING DATE: 1997-12-31
;  EARLIER APPLICATION NUMBER: 08/937,739;  60/025,140
;  EARLIER FILING DATE: 1997-07-25; 1996-07-26
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: Macintosh Wordperfect converted to PC ASCII Text
; SEQ ID NO 23
;    LENGTH: 491
;    TYPE: PRT
;    ORGANISM: Nicotiana tabacum
US-09-001-826-23

  Query Match             55.2%;  Score 32;  DB 2;  Length 491;
  Best Local Similarity   71.4%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        422 RTIVFPT 428


RESULT 18
US-09-352-159-17
; Sequence 17, Application US/09352159A
;.Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;    LENGTH: 554
;    TYPE: PRT
;    ORGANISM: Exophiala spinifera
;    FEATURE:
;    NAME/KEY: SIGNAL
;    LOCATION: (1)...(89)
US-09-352-159-17

  Query Match             55.2%;  Score 32;  DB 4;  Length 554;
  Best Local Similarity   55.6%;  Pred. No. 2.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        362 TTLYPTLTF 370


RESULT 19
US-09-352-168-17
; Sequence 17, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Folkerts, Otto
;  APPLICANT: Gilliam, Jacob T.
```

```
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/352,168A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 554
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(89)
;   OTHER INFORMATION: yeast alpha mating factor secretion signal.
US-09-352-168-17

  Query Match             55.2%;  Score 32;  DB 4;  Length 554;
  Best Local Similarity   55.6%;  Pred. No. 2.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        362 TTLYPTLTF 370


RESULT 20
US-09-486-382B-2
; Sequence 2, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
;  APPLICANT: Hokko Chemical Industry Co., Ltd.
;  APPLICANT:  MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
;  TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
;  TITLE OF INVENTION:  synthase of rice, and DNAs related to said genes
;  FILE REFERENCE: 10647
;  CURRENT APPLICATION NUMBER: US/09/486,382B
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: JP 9-235049
;  PRIOR FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 577
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-09-486-382B-2

  Query Match             55.2%;  Score 32;  DB 4;  Length 577;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        508 RTIVFPT 514


RESULT 21
US-09-486-382B-13
; Sequence 13, Application US/09486382B
; Patent No. 6388174
; GENERAL INFORMATION:
;  APPLICANT: Hokko Chemical Industry Co., Ltd.
;  APPLICANT:  MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES
;  TITLE OF INVENTION: Genes for encoding alpha-subunits of anthranilate
;  TITLE OF INVENTION:  synthase of rice, and DNAs related to said genes
;  FILE REFERENCE: 10647
;  CURRENT APPLICATION NUMBER: US/09/486,382B
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: JP 9-235049
;  PRIOR FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 577
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Modified amino acid sequence of Sequence No. 6388174 2
; Patent No. 6388174
US-09-486-382B-13

  Query Match             55.2%;  Score 32;  DB 4;  Length 577;
  Best Local Similarity   71.4%;  Pred. No. 2.6e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        508 RTIVFPT 514


RESULT 22
US-08-604-789B-3
; Sequence 3, Application US/08604789B
; Patent No. 6118047
;   GENERAL INFORMATION:
;        APPLICANT: Anderson, P.C.
;                   Chomet, P.S.
;                   Griffor, M.C.
;                   Kriz, A.L.
;        TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
;                            AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
;                            OVERPRODUCTION
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
;             STREET: P.O. Box 2938
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/604,789B
;             FILING DATE: 19-Jan-1996
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: <Unknown>
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Woessner, Warren D.
;             REGISTRATION NUMBER: 30,440
;             REFERENCE/DOCKET NUMBER: 950.026US1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (612) 373-6903
;             TELEFAX: (612) 339-3061
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 595 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-604-789B-3

  Query Match             55.2%;  Score 32;  DB 3;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 RTVVYPT 7
              ||:|:||
Db        526 RTIVFPT 532


RESULT 23
US-09-312-721A-3
; Sequence 3, Application US/09312721A
; Patent No. 6271016
;   GENERAL INFORMATION:
;        APPLICANT: Anderson, P.C.
;                   Chomet, P.S.
;                   Griffor, M.C.
;                   Kriz, A.L.
;        TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
;                            AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
;                            OVERPRODUCTION
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
;             STREET: P.O. Box 2938
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/312,721A
;             FILING DATE: 17-May-1999
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/604,789
;             FILING DATE: 19-JAN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Woessner, Warren D.
;             REGISTRATION NUMBER: 30,440
;             REFERENCE/DOCKET NUMBER: 950.026US2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (612) 373-6903
;             TELEFAX: (612) 339-3061
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 595 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-312-721A-3

  Query Match             55.2%;  Score 32;  DB 4;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        526 RTIVFPT 532


RESULT 24
US-09-352-159-40
; Sequence 40, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
;   LENGTH: 598
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (216)...(216)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-352-159-40

  Query Match             55.2%;  Score 32;  DB 4;  Length 598;
  Best Local Similarity   55.6%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        406 TTLYPTLTF 414


RESULT 25
US-09-352-159-23
; Sequence 23, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jonathan P.
;  APPLICANT: Gilliam, Jacob T.
;  APPLICANT: Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 1134
;  CURRENT APPLICATION NUMBER: US/09/352,159A
;  CURRENT FILING DATE: 1999-07-12
;  EARLIER APPLICATION NUMBER: 60/092,936
;  EARLIER FILING DATE: 1998-07-25
;  EARLIER APPLICATION NUMBER: 60/135,391
;  EARLIER FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-352-159-23

  Query Match             55.2%;  Score 32;  DB 4;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        408 TTLYPTLTF 416


Search completed: July 16, 2003, 14:38:04
Job time : 16 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:33:19 ; Search time 27.6667 Seconds
(without alignments)
47.218 Million cell updates/sec

Title: US-09-923-716C-4
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published_Applications_AA:*
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9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	58.6	322	9	US-10-183-116-16	Sequence 16, Appl
2	34	58.6	322	9	US-10-079-384-4	Sequence 4, Appli
3	34	58.6	600	9	US-10-072-307-28	Sequence 28, Appl
4	34	58.6	600	9	US-10-072-307-30	Sequence 30, Appl
5	34	58.6	600	9	US-10-072-307-35	Sequence 35, Appl
6	34	58.6	600	9	US-10-072-307-37	Sequence 37, Appl
7	34	58.6	600	9	US-10-072-307-40	Sequence 40, Appl
8	34	58.6	600	9	US-10-072-307-43	Sequence 43, Appl
9	34	58.6	600	9	US-10-072-307-60	Sequence 60, Appl
10	34	58.6	600	9	US-10-072-307-64	Sequence 64, Appl
11	33	56.9	600	9	US-10-072-307-62	Sequence 62, Appl
12	33	56.9	656	9	US-09-738-626-4577	Sequence 4577, Ap
13	32	55.2	447	9	US-10-169-048-34	Sequence 34, Appl
14	32	55.2	447	9	US-10-169-048-44	Sequence 44, Appl
15	32	55.2	462	9	US-09-770-564-6	Sequence 6, Appli
16	32	55.2	462	9	US-09-770-564-8	Sequence 8, Appli
17	32	55.2	463	9	US-10-072-307-46	Sequence 46, Appl
18	32	55.2	463	9	US-10-072-307-47	Sequence 47, Appl
19	32	55.2	463	9	US-10-072-307-48	Sequence 48, Appl
20	32	55.2	463	9	US-10-072-307-50	Sequence 50, Appl
21	32	55.2	463	9	US-09-770-564-11	Sequence 11, Appl
22	32	55.2	487	9	US-09-770-564-21	Sequence 21, Appl
23	32	55.2	539	9	US-10-072-307-34	Sequence 34, Appl
24	32	55.2	554	9	US-09-770-564-17	Sequence 17, Appl
25	32	55.2	595	10	US-09-733-300-3	Sequence 3, Appli
26	32	55.2	600	9	US-10-072-307-26	Sequence 26, Appl
27	32	55.2	600	9	US-10-072-307-27	Sequence 27, Appl
28	32	55.2	600	9	US-10-072-307-29	Sequence 29, Appl
29	32	55.2	600	9	US-10-072-307-31	Sequence 31, Appl
30	32	55.2	600	9	US-10-072-307-32	Sequence 32, Appl
31	32	55.2	600	9	US-10-072-307-33	Sequence 33, Appl
32	32	55.2	600	9	US-10-072-307-36	Sequence 36, Appl
33	32	55.2	600	9	US-10-072-307-38	Sequence 38, Appl
34	32	55.2	600	9	US-10-072-307-41	Sequence 41, Appl
35	32	55.2	600	9	US-10-072-307-42	Sequence 42, Appl
36	32	55.2	600	9	US-10-072-307-44	Sequence 44, Appl
37	32	55.2	600	9	US-10-072-307-45	Sequence 45, Appl
38	32	55.2	600	9	US-10-072-307-52	Sequence 52, Appl
39	32	55.2	600	9	US-10-072-307-54	Sequence 54, Appl
40	32	55.2	600	9	US-10-072-307-56	Sequence 56, Appl
41	32	55.2	600	9	US-10-072-307-58	Sequence 58, Appl
42	32	55.2	600	9	US-10-072-307-66	Sequence 66, Appl
43	32	55.2	600	9	US-09-770-564-23	Sequence 23, Appl
44	32	55.2	692	9	US-09-770-564-19	Sequence 19, Appl
45	32	55.2	829	9	US-09-770-564-33	Sequence 33, Appl
46	32	55.2	991	9	US-09-770-564-27	Sequence 27, Appl
47	32	55.2	1000	9	US-09-770-564-25	Sequence 25, Appl
48	32	55.2	1196	9	US-09-770-564-31	Sequence 31, Appl
49	32	55.2	1205	9	US-09-770-564-29	Sequence 29, Appl
50	31	53.4	57	10	US-09-864-761-47860	Sequence 47860, A
51	31	53.4	58	9	US-09-764-891-2918	Sequence 2918, Ap
52	31	53.4	157	9	US-09-992-598-103	Sequence 103, App
53	31	53.4	157	9	US-09-989-293A-103	Sequence 103, App
54	31	53.4	157	9	US-09-989-735-103	Sequence 103, App
55	31	53.4	157	9	US-09-990-444-103	Sequence 103, App
56	31	53.4	157	9	US-09-989-730-103	Sequence 103, App
57	31	53.4	157	9	US-09-990-436-103	Sequence 103, App
58	31	53.4	157	9	US-09-991-181-103	Sequence 103, App
59	31	53.4	157	9	US-09-993-687-103	Sequence 103, App
60	31	53.4	157	9	US-09-989-734-103	Sequence 103, App
61	31	53.4	157	9	US-09-997-653-103	Sequence 103, App
62	31	53.4	157	9	US-10-174-590-90	Sequence 90, Appl
63	31	53.4	157	9	US-10-176-758-90	Sequence 90, Appl
64	31	53.4	157	9	US-10-175-737-90	Sequence 90, Appl
65	31	53.4	157	9	US-09-993-667-103	Sequence 103, App
66	31	53.4	157	9	US-10-173-706-90	Sequence 90, Appl
67	31	53.4	157	9	US-10-175-738-90	Sequence 90, Appl
68	31	53.4	157	9	US-10-175-752-90	Sequence 90, Appl
69	31	53.4	157	9	US-10-176-482-90	Sequence 90, Appl
70	31	53.4	157	9	US-10-176-757-90	Sequence 90, Appl
71	31	53.4	157	9	US-10-176-913-90	Sequence 90, Appl
72	31	53.4	157	9	US-10-180-552-90	Sequence 90, Appl
73	31	53.4	157	9	US-10-180-557-90	Sequence 90, Appl
74	31	53.4	157	9	US-09-990-438-103	Sequence 103, App
75	31	53.4	157	9	US-09-990-562-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-10-183-116-16
; Sequence 16, Application US/10183116
; Publication No. US20030092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzhong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CP1

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;  CURRENT APPLICATION NUMBER: US/10/183,116
;  CURRENT FILING DATE:  2002-06-26
;  PRIOR APPLICATION NUMBER: US 60/222,344
;  PRIOR FILING DATE: 2000-08-01
;  PRIOR APPLICATION NUMBER: US 60/202,027
;  PRIOR FILING DATE: 2000-05-04
;  PRIOR APPLICATION NUMBER: US 09/704,707
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: US 60/285,493
;  PRIOR FILING DATE: 2001-04-19
;  PRIOR APPLICATION NUMBER: US 09/849,869
;  PRIOR FILING DATE: 2001-05-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-183-116-16

  Query Match             58.6%;  Score 34;  DB 9;  Length 322;
  Best Local Similarity   62.5%;  Pred. No. 96;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              ::|| |||
Db         97 ILYPVMMF 104


RESULT 2
US-10-079-384-4
; Sequence 4, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
;  APPLICANT: Communi, Didier
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: 9409/2132
;  CURRENT APPLICATION NUMBER: US/10/079,384
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: US 09/885,453
;  PRIOR FILING DATE: 2001-06-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-079-384-4

  Query Match             58.6%;  Score 34;  DB 9;  Length 322;
  Best Local Similarity   62.5%;  Pred. No. 96;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              ::|| |||
Db         97 ILYPVMMF 104


RESULT 3
US-10-072-307-28
; Sequence 28, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 28
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_F7
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-28

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 4
US-10-072-307-30
; Sequence 30, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 30
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_G11
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-30

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 5
US-10-072-307-35
; Sequence 35, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
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;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 35
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F15C3
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-35

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 6
US-10-072-307-37
; Sequence 37, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 37
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F19F2
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-37

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 7
US-10-072-307-40
; Sequence 40, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 40
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F24F2
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-40

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 8
US-10-072-307-43
; Sequence 43, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 43
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F3B5
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-43

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 9
US-10-072-307-60
; Sequence 60, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 60
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;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 215
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 216
;   OTHER INFORMATION: Xaa = Gln, His
US-10-072-307-60

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 10
US-10-072-307-64
; Sequence 64, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 64
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 13
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 403
;   OTHER INFORMATION: Xaa = Val, Leu, Met
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 404
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 419
;   OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 433
;   OTHER INFORMATION: Xaa = Val, Leu, Met
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 443
;   OTHER INFORMATION: Xaa = Ter, Cys, Trp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 478
;   OTHER INFORMATION: Xaa = Leu, Ter, Ser, Trp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 489
;   OTHER INFORMATION: Xaa = Ter, Arg, Gly
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 538
;   OTHER INFORMATION: Xaa = Ter, Arg, Gly
US-10-072-307-64

  Query Match             58.6%;  Score 34;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TTLYPTLIF 416


RESULT 11
US-10-072-307-62
; Sequence 62, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 62
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Rhinocladiella atrovirens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 187
;   OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 209
;   OTHER INFORMATION: Xaa = Ile, Val, Leu, Phe
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 244
;   OTHER INFORMATION: Xaa = Glu, Asp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 262
;   OTHER INFORMATION: Xaa = Ter, Cys, Trp
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 295
;   OTHER INFORMATION: Xaa = Tyr, Asn, Asp, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 299
;   OTHER INFORMATION: Xaa = Leu, Arg, Pro, His
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 403
;   OTHER INFORMATION: Xaa = Val, Leu, Met
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 405
;   OTHER INFORMATION: Xaa = Ala, Thr, Pro, Ser
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 409
```

```
;   OTHER INFORMATION: Xaa = Ala, Thr, Ser, Pro
US-10-072-307-62

  Query Match             56.9%;  Score 33;  DB 9;  Length 600;
  Best Local Similarity   55.6%;  Pred. No. 2.9e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||::|
Db        408 TXLYPTLIF 416


RESULT 12
US-09-738-626-4577
; Sequence 4577, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/09/738,626
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4577
;   LENGTH: 656
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-4577

  Query Match             56.9%;  Score 33;  DB 9;  Length 656;
  Best Local Similarity   62.5%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              :: |||||
Db        307 IIMPTMMF 314


RESULT 13
US-10-169-048-34
; Sequence 34, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
;  APPLICANT: Clarke, Edna Elizabeth
;  APPLICANT:  Zhou, Liqing
;  APPLICANT:  Shea, Jacqueline Elizabeth
;  APPLICANT:  Feldman, Robert Graham
;  APPLICANT:  Holden, David William
;  TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their Use
;  FILE REFERENCE: GJE-97
;  CURRENT APPLICATION NUMBER: US/10/169,048
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: PCT/GB00/04997
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-10-169-048-34

  Query Match             55.2%;  Score 32;  DB 9;  Length 447;
  Best Local Similarity   45.5%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              :|::||   ||
Db        190 QTMIYPFTFFK 200


RESULT 14
US-10-169-048-44
; Sequence 44, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
;  APPLICANT: Clarke, Edna Elizabeth
;  APPLICANT:  Zhou, Liqing
;  APPLICANT:  Shea, Jacqueline Elizabeth
;  APPLICANT:  Feldman, Robert Graham
;  APPLICANT:  Holden, David William
;  TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their
;  FILE REFERENCE: GJE-97
;  CURRENT APPLICATION NUMBER: US/10/169,048
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: PCT/GB00/04997
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-10-169-048-44

  Query Match             55.2%;  Score 32;  DB 9;  Length 447;
  Best Local Similarity   45.5%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              :|::||   ||
Db        190 QTMIYPFTFFK 200


RESULT 15
US-09-770-564-6
; Sequence 6, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-770-564-6
```

```
  Query Match             55.2%;  Score 32;  DB 9;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 16
US-09-770-564-8
; Sequence 8, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
US-09-770-564-8

  Query Match             55.2%;  Score 32;  DB 9;  Length 462;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        270 TTLYPTLTF 278


RESULT 17
US-10-072-307-46
; Sequence 46, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 46
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_TrH1
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-46

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 18
US-10-072-307-47
; Sequence 47, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 47
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_G6
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-47

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 19
US-10-072-307-48
; Sequence 48, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 48
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_H8
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-48

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
```

```
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 20
US-10-072-307-50
; Sequence 50, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 50
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_B6
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-50

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 21
US-09-770-564-11
; Sequence 11, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   OTHER INFORMATION: Extra lysine in the polypeptide sequence of
;   OTHER INFORMATION: K:trAPAO, 463 aa.
US-09-770-564-11

  Query Match             55.2%;  Score 32;  DB 9;  Length 463;
  Best Local Similarity   55.6%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        271 TTLYPTLTF 279


RESULT 22
US-09-770-564-21
; Sequence 21, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(24)
;   OTHER INFORMATION: K:trAPAO translational fusion with barley alpha
;   OTHER INFORMATION: amylase signal sequence, for expression and
;   OTHER INFORMATION: secretion of the mature trAPAO in maize.
US-09-770-564-21

  Query Match             55.2%;  Score 32;  DB 9;  Length 487;
  Best Local Similarity   55.6%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        295 TTLYPTLTF 303


RESULT 23
US-10-072-307-34
; Sequence 34, Application US/10072307
; Publication No. US20030056245A1
; GENERAL INFORMATION:
;  APPLICANT: Chatterjee, Ranjini
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  English, James
;  TITLE OF INVENTION: AP1 Amine Oxidase Variants
;  FILE REFERENCE: 02-10402US
;  CURRENT APPLICATION NUMBER: US/10/072,307
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: US 60/266,918
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: US 60/300,324
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 34
;   LENGTH: 539
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: LIMS-SeqID Translation_of_4F15A11
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-072-307-34

  Query Match             55.2%;  Score 32;  DB 9;  Length 539;
  Best Local Similarity   55.6%;  Pred. No. 3.9e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        347 TTLYPTLTF 355


RESULT 24
US-09-770-564-17
; Sequence 17, Application US/09770564
; Publication No. US20030126636A1
; GENERAL INFORMATION:
;  APPLICANT: Crasta, Oswald R.
;  APPLICANT:  Duvick, Jonathan P.
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Gilliam, Jacob T.
;  APPLICANT:  Maddox, Joyce R.
;  TITLE OF INVENTION: Amino Polyol Amine Oxidase
;  TITLE OF INVENTION:  Polynucleotides and Related Polypeptides and Methods of Use
;  FILE REFERENCE: 0875
;  CURRENT APPLICATION NUMBER: US/09/770,564
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 09/352,168
;  PRIOR FILING DATE: 1999-07-12
;  PRIOR APPLICATION NUMBER: 60/092,936
;  PRIOR FILING DATE: 1998-07-25
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 554
;   TYPE: PRT
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(89)
;   OTHER INFORMATION: yeast alpha mating factor secretion signal.
US-09-770-564-17

  Query Match             55.2%;  Score 32;  DB 9;  Length 554;
  Best Local Similarity   55.6%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | :|||: |
Db        362 TTLYPTLTF 370


RESULT 25
US-09-733-300-3
; Sequence 3, Application US/09733300
; Patent No. US20020061570A1
;   GENERAL INFORMATION:
;        APPLICANT: Anderson, P.C.
;                   Chomet, P.S.
;                   Griffor, M.C.
;                   Kriz, A.L.
;        TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
;                            AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
;                            OVERPRODUCTION
;        NUMBER OF SEQUENCES: 16
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
;             STREET: P.O. Box 2938
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/733,300
;             FILING DATE: 08-Dec-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/312,721
;             FILING DATE: 2000-09-11
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Woessner, Warren D.
;             REGISTRATION NUMBER: 30,440
;             REFERENCE/DOCKET NUMBER: 950.026US2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (612) 373-6903
;             TELEFAX: (612) 339-3061
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 595 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-733-300-3

  Query Match             55.2%;  Score 32;  DB 10;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 4.4e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:||
Db        526 RTIVFPT 532


Search completed: July 16, 2003, 14:39:39
Job time : 27.6667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 20 Seconds
(without alignments)
52.874 Million cell updates/sec

Title: US-09-923-716C-4
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	70.7	333	2	S74406	hypothetical prote
2	41	70.7	974	2	T29545	hypothetical prote
3	38	65.5	262	2	C84800	3-oxo-5-alpha-ster
4	38	65.5	394	2	G86657	ABC transporter AT
5	37	63.8	395	2	H83424	hypothetical prote
6	35	60.3	180	2	D86267	T6J4.4 protein - A
7	35	60.3	435	2	E72342	pmbA-related prote
8	35	60.3	598	2	AG0890	probable arylsulfa
9	35	60.3	887	2	B96598	hypothetical prote
10	34	58.6	303	2	H84758	hypothetical prote
11	34	58.6	347	2	AD3513	channel protein vi
12	34	58.6	373	2	S17955	long-chain-fatty-a
13	34	58.6	373	2	S15161	long-chain-fatty-a
14	34	58.6	389	2	AD0478	acetylornithine de
15	34	58.6	404	2	B41317	O-antigen ligase c
16	34	58.6	404	2	AE0973	O-antigen ligase [
17	34	58.6	464	2	T50785	nucleoid DNA-bindi
18	34	58.6	674	2	D72329	hypothetical prote
19	34	58.6	711	2	A86424	unknown protein, 3
20	33.5	57.8	1724	2	T13942	UNC-13-B protein --
21	33	56.9	120	1	E69798	conserved hypothet
22	33	56.9	136	2	A90710	regulator of nucle
23	33	56.9	136	2	E85560	regulator of nucle
24	33	56.9	136	2	I57917	nucleoside diphosp
25	33	56.9	205	2	S29308	hypothetical prote
26	33	56.9	205	2	F83013	probable transcrip
27	33	56.9	221	2	AH0324	probable transport
28	33	56.9	261	2	T05447	hypothetical prote
29	33	56.9	390	2	AF3425	oxidoreductase (EC
30	33	56.9	394	2	S69870	hypothetical prote
31	33	56.9	531	2	D90453	hypothetical prote
32	33	56.9	551	2	D69282	glutamyl-tRNA synt
33	33	56.9	594	2	S00961	hypothetical prote
34	33	56.9	821	2	B75530	ATP-dependent prot
35	33	56.9	1021	2	T08601	hypothetical prote
36	33	56.9	1235	2	AC1358	ATP-dependent deox
37	33	56.9	1235	2	AC1728	ATP-dependent deox
38	32	55.2	61	1	F2RZKS	photosystem II pro
39	32	55.2	136	2	AC0578	regulator of nucle
40	32	55.2	142	2	G98072	7,8-dihydro-8-oxog
41	32	55.2	143	1	WMBE6H	transcription regu
42	32	55.2	143	2	T43976	transactivator [im
43	32	55.2	169	2	S72166	lipopolysaccharide
44	32	55.2	201	2	T07011	proteinase inhibit
45	32	55.2	203	2	E75413	conserved hypothet
46	32	55.2	214	2	G71318	hypothetical prote
47	32	55.2	214	2	D89985	hypothetical prote
48	32	55.2	214	2	T49174	hypothetical prote
49	32	55.2	283	2	T13879	maturase-like prot
50	32	55.2	283	2	AG1560	hypothetical prote
51	32	55.2	283	2	AI1202	hypothetical prote
52	32	55.2	285	2	T09308	immediate-early pr
53	32	55.2	334	2	T44163	hypothetical prote
54	32	55.2	421	2	S26246	glutamate/aspartat
55	32	55.2	458	2	A96938	polyA polymerase [
56	32	55.2	468	2	A55116	vacuolar ATPase (E
57	32	55.2	513	2	T40998	hypothetical prote
58	32	55.2	526	2	T49199	anthranilate synth
59	32	55.2	543	2	T22585	hypothetical prote
60	32	55.2	564	2	S15962	hypothetical prote
61	32	55.2	595	2	JQ1684	anthranilate synth
62	32	55.2	603	2	T11843	NADH2 dehydrogenas
63	32	55.2	620	2	T21391	hypothetical prote
64	32	55.2	1416	2	D71350	probable DNA-direc
65	32	55.2	1501	2	T29094	ribulose-bisphosph
66	32	55.2	1716	2	T14103	probable DNA-direc
67	32	55.2	3175	1	RRWVEV	genome polyprotein
68	31	53.4	80	2	A60450	hypothetical prote
69	31	53.4	95	2	B83814	Na+/H+ antiporter
70	31	53.4	104	2	T17649	hypothetical prote
71	31	53.4	105	2	T44098	hypothetical prote
72	31	53.4	142	2	G95207	MutT/nudix family
73	31	53.4	185	2	T29063	hypothetical prote
74	31	53.4	207	2	D65095	hypothetical prote
75	31	53.4	207	2	A98123	hypothetical prote

ALIGNMENTS

RESULT 1
S74406
hypothetical protein sll0456 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S74406
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74406
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-333 <KAN>
A;Cross-references: EMBL:D64001; GB:AB001339; NID:g1001102; PIDN:BAA10324.1; PID:d101
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 70.7%; Score 41; DB 2; Length 333;
Best Local Similarity 77.8%; Pred. No. 2.8;

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  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |||||||::|
Db        172 TVVYPTLVF 180


RESULT 2
T29545
hypothetical protein F48C1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29545
R;Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid F48C1.
A;Reference number: Z20638
A;Accession: T29545
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-974 <GAT>
A;Cross-references: EMBL:U97015; PIDN:AAB52345.1; GSPDB:GN00019; CESP:F48C1.1
A;Experimental source: strain Bristol N2; clone F48C1
C;Genetics:
A;Gene: CESP:F48C1.1
A;Map position: 1
A;Introns: 15/2; 58/3; 110/3; 150/1; 176/1; 267/2; 296/2; 326/2; 394/3; 441/1; 550/3; 59

  Query Match             70.7%;  Score 41;  DB 2;  Length 974;
  Best Local Similarity   60.0%;  Pred. No. 8.3;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :|::|| |||
Db        851 QTIIYPPMMF 860


RESULT 3
C84800
3-oxo-5-alpha-steroid 4-dehydrogenase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: C84800
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84800
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-262 <STO>
A;Cross-references: GB:AE002093; NID:g4895180; PIDN:AAD32767.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g38050
A;Map position: 2
C;Superfamily: Caenorhabditis elegans hypothetical protein ZK1251.3

  Query Match             65.5%;  Score 38;  DB 2;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 8.2;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 4
G86657
ABC transporter ATP binding protein ycgB [imported] - Lactococcus lactis subsp. lactis (
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: G86657
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86657
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <STO>
A;Cross-references: GB:AE005176; PID:g12723123; PIDN:AAK04361.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ycgB

  Query Match             65.5%;  Score 38;  DB 2;  Length 394;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |::|||| |
Db         47 TLIYPTMRF 55


RESULT 5
H83424
hypothetical protein PA1765 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83424
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <STO>
A;Cross-references: GB:AE004602; GB:AE004091; NID:g9947739; PIDN:AAG05154.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1765

  Query Match             63.8%;  Score 37;  DB 2;  Length 395;
  Best Local Similarity   60.0%;  Pred. No. 20;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | ||||:::|
Db        292 RQVVYPSLLF 301


RESULT 6
D86267
T6J4.4 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C;Accession: D86267
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86267
A;Status: preliminary
A;Molecule type: DNA
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A;Residues: 1-180 <STO>
A;Cross-references: GB:AE005172; NID:g9958068; PIDN:AAG09557.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

  Query Match             60.3%;  Score 35;  DB 2;  Length 180;
  Best Local Similarity   60.0%;  Pred. No. 21;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        124 RQLVYPTKLF 133


RESULT 7
E72342
pmbA-related protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72342
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: E72342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-435 <ARN>
A;Cross-references: GB:AE001743; GB:AE000512; NID:g4981241; PIDN:AAD35809.1; PID:g498125
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0727
C;Superfamily: Escherichia coli pmbA protein

  Query Match             60.3%;  Score 35;  DB 2;  Length 435;
  Best Local Similarity   54.5%;  Pred. No. 53;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | |: ||:|:|
Db        135 RVVMVPTVMYK 145


RESULT 8
AG0890
probable arylsulfate sulfotransferase [imported] - Salmonella enterica subsp. enterica s
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AG0890
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AG0890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-598 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07717.1; PID:g16504269; GSPDB:GN00176
C;Genetics:
A;Gene: STY3370

  Query Match             60.3%;  Score 35;  DB 2;  Length 598;
  Best Local Similarity   66.7%;  Pred. No. 73;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              :|:|| |||
Db        590 LVHPTQMFK 598


RESULT 9
B96598
hypothetical protein T5A14.3 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96598
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-887 <STO>
A;Cross-references: GB:AE005173; NID:g4204259; PIDN:AAD10640.1; GSPDB:GN00141
C;Genetics:
A;Gene: T5A14.3
A;Map position: 1

  Query Match             60.3%;  Score 35;  DB 2;  Length 887;
  Best Local Similarity   70.0%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              ||| ||:| |
Db        696 TVVNPTLMLK 705


RESULT 10
H84758
hypothetical protein At2g34620 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84758
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84758
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <STO>
A;Cross-references: GB:AE002093; NID:g3128213; PIDN:AAC26693.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g34620
A;Map position: 2

  Query Match             58.6%;  Score 34;  DB 2;  Length 303;
  Best Local Similarity   60.0%;  Pred. No. 57;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              || :||  ||
Db        120 RTELYPVFMF 129


RESULT 11
AD3513
channel protein virB6 homolog [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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C;Accession: AD3513
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AD3513
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53271.1; PID:g17984152; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0030
A;Map position: II

  Query Match            58.6%;  Score 34;  DB 2;  Length 347;
  Best Local Similarity  60.0%;  Pred. No. 65;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |:| | ||:|
Db        257 TIVMPYMMYK 266


RESULT 12
S17955
long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium lei
C;Species: Photobacterium leiognathi
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 03-Jun-2002
C;Accession: S17955
R;Lee, C.Y.; Szittner, R.B.; Meighen, E.A.
Eur. J. Biochem. 201, 161-167, 1991
A;Title: The lux genes of the luminous bacterial symbiont, Photobacterium leiognathi, of
coli.
A;Reference number: S17836; MUID:92007870; PMID:1915359
A;Accession: S17955
A;Molecule type: DNA
A;Residues: 1-373 <LEE>
A;Cross-references: EMBL:M63594; NID:g150687; PIDN:AAA25620.1; PID:g150692
C;Genetics:
A;Gene: luxE
C;Keywords: acid-thiol ligase
F;364/Active site: Cys (covalent substrate-binding) #status predicted

  Query Match            58.6%;  Score 34;  DB 2;  Length 373;
  Best Local Similarity  75.0%;  Pred. No. 70;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              |:|| |||
Db         78 VFPTSMFK 85


RESULT 13
S15161
long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) luxE - Photobacterium pho
N;Alternate names: acyl-protein synthetase
C;Species: Photobacterium phosphoreum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
C;Accession: S15161
R;Soly, R.R.; Meighen, E.A.
J. Mol. Biol. 219, 69-77, 1991
A;Title: Identification of the acyl transfer site of fatty acyl-protein synthetase from
A;Reference number: S15160; MUID:91218179; PMID:2023262
A;Accession: S15161
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-373 <JMO>
C;Genetics:
A;Gene: luxE
C;Keywords: acid-thiol ligase
F;364/Active site: Cys (covalent substrate-binding) #status predicted

  Query Match            58.6%;  Score 34;  DB 2;  Length 373;
  Best Local Similarity  75.0%;  Pred. No. 70;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              |:|| |||
Db         78 VFPTSMFK 85


RESULT 14
AD0478
acetylornithine deacetylase (EC 3.5.1.16) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
C;Accession: AD0478
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0478
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC93392.1; PID:g15981838; GSPDB:GN00175
C;Genetics:
A;Gene: argE
C;Superfamily: succinyl-diaminopimelate desuccinylase
C;Keywords: hydrolase

  Query Match            58.6%;  Score 34;  DB 2;  Length 389;
  Best Local Similarity  66.7%;  Pred. No. 73;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |: |||| |
Db        238 TIPYPTMNF 246


RESULT 15
B41317
O-antigen ligase complex protein rfaL - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 08-Oct-1999
C;Accession: B41317
R;MacLachlan, P.R.; Kadam, S.K.; Sanderson, K.E.
J. Bacteriol. 173, 7151-7163, 1991
A;Title: Cloning, characterization, and DNA sequence of the rfaLK region for lipopoly
A;Reference number: A41317; MUID:92041612; PMID:1657881
A;Accession: B41317
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <MAC>
A;Cross-references: GB:M73826; NID:g154328; PIDN:AAA27206.1; PID:g154330
C;Keywords: transmembrane protein

  Query Match            58.6%;  Score 34;  DB 2;  Length 404;
  Best Local Similarity  63.6%;  Pred. No. 76;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | |||  ||
Db        305 RVVDYPTWTFK 315


RESULT 16
AE0973
O-antigen ligase [imported] - Salmonella enterica subsp. enterica serovar Typhi (stra
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
```

```
C;Accession: AE0973
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AE0973
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03281.1; PID:g16504902; GSPDB:GN00176
C;Genetics:
A;Gene: waaL

  Query Match             58.6%;  Score 34;  DB 2;  Length 404;
  Best Local Similarity   63.6%;  Pred. No. 76;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | |||  ||
Db        305 RVVDYPTWTFK 315


RESULT 17
T50785
nucleoid DNA-binding protein cnd41-like protein - Arabidopsis thaliana
N;Alternate names: protein T30N20_30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50785
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25240
A;Accession: T50785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <BEV>
A;Cross-references: EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
C;Genetics:
A;Map position: 5
A;Introns: 58/1
A;Note: T30N20_30

  Query Match             58.6%;  Score 34;  DB 2;  Length 464;
  Best Local Similarity   66.7%;  Pred. No. 88;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              || |||: |
Db        392 TVTYPTIAF 400


RESULT 18
D72329
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72329
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72329
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-674 <ARN>
A;Cross-references: GB:AE001749; GB:AE000512; NID:g4981346; PIDN:AAD35899.1; PID:g498134
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0817

  Query Match             58.6%;  Score 34;  DB 2;  Length 674;
  Best Local Similarity   60.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :| |||  ||
Db        192 QTFVYPVFMF 201


RESULT 19
A86424
unknown protein, 35070-37205 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86424
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-711 <STO>
A;Cross-references: GB:AE005172; NID:g10092467; PIDN:AAG12869.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

  Query Match             58.6%;  Score 34;  DB 2;  Length 711;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |:|||: :
Db        461 RRVIYPTLRY 470


RESULT 20
T13942
UNC-13-B protein - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13942
R;Xu, X.Z.; Wes, P.D.; Chen, H.; Li, H.S.; Yu, M.; Morgan, S.; Liu, Y.; Montell, C.
J. Biol. Chem. 273, 31297, 1998
A;Title: Retinal targets for calmodulin include proteins implicated in synaptic trans
A;Reference number: Z17709; MUID:99030403; PMID:9813038
A;Accession: T13942
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1724 <XUX>
A;Cross-references: EMBL:Y17922; NID:g3893112; PIDN:CAA76942.1; PID:g3893113
C;Genetics:
A;Cross-references: FlyBase:FBgn0025726
A;Note: UNC-13-B
C;Superfamily: protein kinase C zinc-binding repeat homology
F;602-651/Domain: protein kinase C zinc-binding repeat homology <KZN>

  Query Match             57.8%;  Score 33.5;  DB 2;  Length 1724;
  Best Local Similarity   50.0%;  Pred. No. 4.2e+02;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    5;  Gaps    1;

Qy          1 RTVVYP-----TMMFK 11
              :|:| |     |||||
```

```
Db       1437 KTIVLPPMTDKTMMFK 1452


RESULT 21
E69798
conserved hypothetical protein yetH - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: E69798
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69798
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-120 <KUN>
A;Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12535.1; PID:g2633029
A;Experimental source: strain 168
C;Genetics:
A;Gene: yetH
C;Superfamily: Bacillus probable methylglyoxalase yurT

  Query Match             56.9%;  Score 33;  DB 1;  Length 120;
  Best Local Similarity   54.5%;  Pred. No. 34;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | |:||  | |
Db         53 RLVIYPKAMMK 63


RESULT 22
A90710
regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157:H7
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: A90710
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A90710
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34072.1; PID:g13360107; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0649

  Query Match             56.9%;  Score 33;  DB 2;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 23
E85560
regulator of nucleoside diphosphate kinase [imported] - Escherichia coli (strain O157
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E85560
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85560
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <STO>
A;Cross-references: GB:AE005174; NID:g12513506; PIDN:AAG54945.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: rnk

  Query Match             56.9%;  Score 33;  DB 2;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 24
I57917
nucleoside diphosphate kinase regulator - Escherichia coli (strain K-12)
N;Alternate names: rnk protein
C;Species: Escherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 01-Mar-2002
C;Accession: I57917; H64794
R;Schlictman, D.; Shankar, S.; Chakrabarty, A.M.
Mol. Microbiol. 16, 309-320, 1995
A;Title: The Escherichia coli genes sspA and rnk can functionally replace the Pseudom
A;Reference number: I57917; MUID:96015444; PMID:7565093
A;Accession: I57917
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-136 <RES>
A;Cross-references: GB:L37900; NID:g598117; PIDN:AAC36933.1; PID:g598118
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64794
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-136 <BLAT>
A;Cross-references: GB:AE000166; GB:U00096; NID:g1786819; PIDN:AAC73711.1; PID:g17868
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: rnk

  Query Match             56.9%;  Score 33;  DB 2;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 25
S29308
hypothetical protein 3 (phaC2 3' region) - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999
```

C;Accession: S29308; S28380
R;Timm, A.; Steinbuechel, A.
Eur. J. Biochem. 209, 15-30, 1992
A;Title: Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid) gene locus c
A;Reference number: S29303; MUID:93011120; PMID:1396693
A;Accession: S29308
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <TIM>
A;Cross-references: EMBL:X66592; NID:g45388; PIDN:CAA47154.1; PID:g45394

Query Match 56.9%; Score 33; DB 2; Length 205;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 RTVVYPTMM 9
              ||||| ||
Db        172 RTVVYQIMM 180
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Search completed: July 16, 2003, 14:34:16
Job time : 20 secs

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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:44 ; Search time 10.3333 Seconds
(without alignments)
44.152 Million cell updates/sec

Title: US-09-923-716C-4
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	65.5	262	1	DET2_ARATH	Q38944 arabidopsis
2	34	58.6	373	1	LUXE_PHOLE	P29334 photobacter
3	34	58.6	404	1	RFAL_SALTY	P26471 salmonella
4	33	56.9	136	1	RNK_ECOLI	P40679 escherichia
5	33	56.9	193	1	RCF1_DICDI	O96390 dictyosteli
6	33	56.9	551	1	SYE_ARCFU	O29979 archaeoglob
7	33	56.9	594	1	YKP3_KLULA	P05469 kluyveromyc
8	32	55.2	61	1	PSBK_ORYSA	P12162 oryza sativ
9	32	55.2	61	1	PSBK_WHEAT	P58273 triticum ae
10	32	55.2	143	1	B701_HSV6G	P30024 human herpe
11	32	55.2	169	1	COAD_CHRVI	P71154 chromatium
12	32	55.2	200	1	CAKB_COTJA	Q98855 coturnix co
13	32	55.2	201	1	IP23_LYCES	Q43502 lycopersico
14	32	55.2	214	1	Y473_TREPA	O83486 treponema p
15	32	55.2	421	1	GLTT_BACCA	P24944 bacillus ca
16	32	55.2	468	1	VAS1_BOVIN	P40682 bos taurus
17	32	55.2	595	1	TRPE_ARATH	P32068 arabidopsis
18	32	55.2	603	1	NU5M_HYLLA	P03919 hylobates l
19	32	55.2	1416	1	RPOC_TREPA	O83270 treponema p
20	32	55.2	1716	1	RPA1_RAT	O54889 rattus norv
21	32	55.2	3175	1	RPOA_EAV	P19811 equine arte
22	31	53.4	157	1	SMP1_HUMAN	O95807 homo sapien
23	31	53.4	207	1	YQJI_ECOLI	Q46872 escherichia
24	31	53.4	320	1	DNC_HUMAN	Q9hc21 homo sapien
25	31	53.4	362	1	MSP1_YEAST	P28737 saccharomyc
26	31	53.4	421	1	GLTT_BACST	P24943 bacillus st
27	31	53.4	437	1	SECY_BUCAI	P57571 buchnera ap
28	31	53.4	439	1	RHG1_HUMAN	Q07960 homo sapien
29	31	53.4	440	1	AK_CHLPN	Q9z610 chlamydia p
30	31	53.4	442	1	SECY_SYNY3	P77964 synechocyst
31	31	53.4	507	1	PDI_DATGL	Q9xf61 datisca glo
32	31	53.4	527	1	KITH_HSVSA	P21293 herpesvirus
33	31	53.4	601	1	NU5M_DASNO	O21335 dasypus nov
34	31	53.4	604	1	NU5M_HORSE	P48656 equus cabal
35	31	53.4	606	1	NU5M_BOVIN	P03920 bos taurus
36	31	53.4	606	1	NU5M_CERSI	O03205 ceratotheri
37	31	53.4	606	1	NU5M_EQUAS	P92485 equus asinu
38	31	53.4	606	1	NU5M_SHEEP	O78756 ovis aries
39	31	53.4	640	1	GIDA_ANASP	Q8yr87 anabaena sp
40	31	53.4	657	1	UVRB_CAMJE	Q9ppm7 campylobact
41	31	53.4	714	1	PBPF_BACSU	P38050 bacillus su
42	31	53.4	1067	1	EG52_XENLA	Q91783 xenopus lae
43	31	53.4	3358	1	PGCV_MOUSE	Q62059 mus musculu
44	31	53.4	4196	1	DYHC_SCHPO	O13290 schizosacch
45	30.5	52.6	1968	1	RRPO_PVMR	P17965 potato viru
46	30	51.7	61	1	PSBK_HORVU	P25877 hordeum vul
47	30	51.7	116	1	LUXE_PHOLU	P19842 photorhabdu
48	30	51.7	122	1	YJ41_YEAST	P47121 saccharomyc
49	30	51.7	149	1	YQBN_BACSU	P45930 bacillus su
50	30	51.7	158	1	IP2X_SOLTU	Q00782 solanum tub
51	30	51.7	193	1	RCF2_DICDI	Q9gps3 dictyosteli
52	30	51.7	221	1	KCY1_BORBU	O51154 borrelia bu
53	30	51.7	238	1	YG26_HAEIN	P44278 haemophilus
54	30	51.7	265	1	UL07_HSVSA	Q01028 herpesvirus
55	30	51.7	315	1	VC04_VACCV	P17370 vaccinia vi
56	30	51.7	316	1	VC04_VACCC	P21038 vaccinia vi
57	30	51.7	316	1	VC04_VARV	P34012 variola vir
58	30	51.7	352	1	GLN1_DAUCA	O22504 daucus caro
59	30	51.7	356	1	GLN1_MEDSA	P04078 medicago sa
60	30	51.7	356	1	GLN1_PHAVU	P04770 phaseolus v
61	30	51.7	356	1	GLNA_VIGAC	P32289 vigna aconi
62	30	51.7	358	1	GLNA_LACSA	P23712 lactuca sat
63	30	51.7	376	1	YG3W_YEAST	P53293 saccharomyc
64	30	51.7	378	1	LUXE_VIBHA	P14286 vibrio harv
65	30	51.7	416	1	PXN1_XENLA	P49263 xenopus lae
66	30	51.7	420	1	PUR2_LISIN	Q92ap4 listeria in
67	30	51.7	420	1	PUR2_LISMO	Q8y6c6 listeria mo
68	30	51.7	426	1	STE2_SACKL	P12384 saccharomyc
69	30	51.7	477	1	LYII_HUMAN	Q14108 homo sapien
70	30	51.7	477	1	LYII_RAT	P27615 rattus norv
71	30	51.7	497	1	YJ92_YEAST	P47158 saccharomyc
72	30	51.7	519	1	SNX2_HUMAN	O60749 homo sapien
73	30	51.7	519	1	SNX2_MOUSE	Q9cwk8 mus musculu
74	30	51.7	521	1	PEL1_SACPS	P79001 saccharomyc
75	30	51.7	536	1	CCA4_DROME	Q9ve00 drosophila

ALIGNMENTS

RESULT 1
DET2_ARATH
ID DET2_ARATH STANDARD; PRT; 262 AA.
AC Q38944; Q9SH83;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable steroid reductase DET2 (EC 1.3.99.-).
GN DET2 OR AT2G38050 OR T8P21.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=96185496; PubMed=8602526;
RA Li J., Nagpal P., Vitart V., McMorris T.C., Chory J.;
RT "A role for brassinosteroids in light-dependent development of
RT Arabidopsis.";
RL Science 272:398-401(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;

```
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RA   Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT   "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT   SSP consortium (Salk/Stanford/PGEC).";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Probably involved in a reduction step in the
CC       biosynthesis of the plant steroid, brassinolide. Defects in DET2
CC       leads to defects in light-regulated development.
CC   -!- PATHWAY: Brassinolide biosynthesis.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE STEROID 5-ALPHA REDUCTASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U53860; AAC49264.1; -.
DR   EMBL; AC007661; AAD32767.1; -.
DR   EMBL; AY045926; AAK76600.1; -.
DR   EMBL; AY079337; AAL85068.1; -.
DR   InterPro; IPR001104; Strd5A_dhC.
DR   Pfam; PF02544; Steroid_dh; 1.
DR   PROSITE; PS50244; S5A_REDUCTASE; 1.
KW   Oxidoreductase; Transmembrane.
FT   TRANSMEM     13     33       POTENTIAL.
FT   TRANSMEM     51     71       POTENTIAL.
FT   TRANSMEM    113    133       POTENTIAL.
FT   TRANSMEM    148    168       POTENTIAL.
FT   TRANSMEM    205    225       POTENTIAL.
FT   CONFLICT    198    198       C -> R (IN REF. 1).
SQ   SEQUENCE   262 AA;  30635 MW;  88291B8A8AF55664 CRC64;

  Query Match             65.5%;  Score 38;  DB 1;  Length 262;
  Best Local Similarity   45.5%;  Pred. No. 1.8;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              ||::||  :|:
Db         93 RTIIYPLRLFR 103


RESULT 2
LUXE_PHOLE
ID   LUXE_PHOLE     STANDARD;      PRT;   373 AA.
AC   P29334;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE   protein synthetase).
GN   LUXE.
OS   Photobacterium leiognathi.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
OC   Photobacterium.
OX   NCBI_TaxID=658;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 25521;
RX   MEDLINE=92007870; PubMed=1915359;
RA   Lee C.Y., Szittner R.B., Meighen E.A.;
RT   "The lux genes of the luminous bacterial symbiont, Photobacterium
RT   leiognathi, of the ponyfish. Nucleotide sequence, difference in gene
RT   organization, and high expression in mutant Escherichia coli.";
RL   Eur. J. Biochem. 201:161-167(1991).
CC   -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC       IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC       FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC       SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC   -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC       an acyl-protein thiolester.
CC   -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M63594; AAA25620.1; -.
DR   PIR; S17955; S17955.
KW   Luminescence; Ligase.
SQ   SEQUENCE   373 AA;  43099 MW;  1B31848B00BF9921 CRC64;

  Query Match             58.6%;  Score 34;  DB 1;  Length 373;
  Best Local Similarity   75.0%;  Pred. No. 17;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              |:|| |||
Db         78 VFPTSMFK 85


RESULT 3
RFAL_SALTY
ID   RFAL_SALTY     STANDARD;      PRT;   404 AA.
AC   P26471;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   O-antigen ligase.
GN   RFAL OR WAAL OR RFBT OR STM3713.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RX   MEDLINE=92041612; PubMed=1657881;
RA   Maclachlan P.R., Kadam S.K., Sanderson K.E.;
RT   "Cloning, characterization, and DNA sequence of the rfaLK region for
RT   lipopolysaccharide synthesis in Salmonella typhimurium LT2.";
RL   J. Bacteriol. 173:7151-7163(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
CC   -!- FUNCTION: ADDS THE O-ANTIGEN ON THE GLUCOSE(II) GROUP OF LPS.
CC   -!- PATHWAY: Lipopolysaccharide core biosynthesis.
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CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: SHOWS ALMOST NO SIMILARITY TO E.COLI RFAL.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M73826; AAA27206.1; -.
DR   EMBL; AE008872; AAL22572.1; -.
DR   PIR; B41317; B41317.
DR   StyGene; SG10340; rfaL.
KW   Lipopolysaccharide biosynthesis; Ligase; Transmembrane;
KW   Complete proteome.
FT   TRANSMEM     66     84       POTENTIAL.
FT   TRANSMEM    184    203       POTENTIAL.
FT   TRANSMEM    227    244       POTENTIAL.
SQ   SEQUENCE   404 AA;  46034 MW;  1B84F7B3C757D2AB CRC64;

  Query Match             58.6%;  Score 34;  DB 1;  Length 404;
  Best Local Similarity   63.6%;  Pred. No. 19;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | |||  ||
Db        305 RVVDYPTWTFK 315


RESULT 4
RNK_ECOLI
ID   RNK_ECOLI      STANDARD;      PRT;   136 AA.
AC   P40679;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Regulator of nucleoside diphosphate kinase.
GN   RNK OR B0610 OR Z0754 OR ECS0649.
OS   Escherichia coli, and
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562, 83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96015444; PubMed=7565093;
RA   Schlictman D., Shankar S., Chakrabarty A.M.;
RT   "The Escherichia coli genes sspA and rnk can functionally replace the
RT   Pseudomonas aeruginosa alginate regulatory gene algR2.";
RL   Mol. Microbiol. 16:309-320(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA   Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA   Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97061202; PubMed=8905232;
RA   Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA   Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA   Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA   Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA   Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA   Yano M., Horiuchi T.;
RT   "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT   corresponding to the 12.7-28.0 min region on the linkage map.";
RL   DNA Res. 3:137-155(1996).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
CC   -!- FUNCTION: RNK AND SSPA CAN FUNCTIONALLY REPLACE P.AERUGINOSA
CC       ALGINATE REGULATORY GENE ALGR2.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L37900; AAC36933.1; -.
DR   EMBL; AE000166; AAC73711.1; -.
DR   EMBL; U82598; AAB40810.1; -.
DR   EMBL; D90701; BAA35239.1; -.
DR   EMBL; D90702; BAA35248.1; -.
DR   EMBL; AE005240; AAG54945.1; -.
DR   EMBL; AP002552; BAB34072.1; -.
DR   EcoGene; EG12637; rnk.
KW   Complete proteome.
SQ   SEQUENCE   136 AA;  14927 MW;  7043926623BA5E1E CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 136;
  Best Local Similarity   66.7%;  Pred. No. 9.8;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||:|||  |
Db         73 RTLVYPAKM 81


RESULT 5
RCF1_DICDI
ID   RCF1_DICDI     STANDARD;      PRT;   193 AA.
AC   O96390;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   RAS-related protein racF1.
GN   RACF1.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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```
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99214006; PubMed=10198067;
RA   Rivero F., Albrecht R., Dislich H., Bracco E., Graciotti L.,
RA   Bozzaro S., Noegel A.A.;
RT   "RacF1, a novel member of the Rho protein family in Dictyostelium
RT   discoideum, associates transiently with cell contact areas,
RT   macropinosomes and phagosomes.";
RL   Mol. Biol. Cell 10:1205-1219(1999).
CC   -!- FUNCTION: MIGHT ACT IN CONCERT AND/OR SHARE FUNCTIONS WITH OTHER
CC       MEMBERS OF THE RHO FAMILY IN THE REGULATION OF A SUBSET OF
CC       CYTOSKELETAL REARRANGEMENTS THAT ARE REQUIRED FOR THESE PROCESSES.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound.
CC   -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AF037042; AAD09143.1; -.
DR   HSSP; P21181; 1AM4.
DR   DictyDb; DD?????; racF1.
DR   InterPro; IPR003578; GTPase_Rho.
DR   InterPro; IPR001230; Prenyl_site.
DR   InterPro; IPR001806; Ras_trnsfrmng.
DR   InterPro; IPR005225; Small_GTP.
DR   Pfam; PF00071; ras; 1.
DR   PRINTS; PR00449; RASTRNSFRMNG.
DR   SMART; SM00174; RHO; 1.
DR   TIGRFAMs; TIGR00231; small_GTP; 1.
KW   GTP-binding; Prenylation; Lipoprotein.
FT   NP_BIND      10     17       GTP (BY SIMILARITY).
FT   NP_BIND      57     61       GTP (BY SIMILARITY).
FT   NP_BIND     115    118       GTP (BY SIMILARITY).
FT   DOMAIN       32     40       EFFECTOR REGION (POTENTIAL).
FT   LIPID       190    190       GERANYL-GERANYL (BY SIMILARITY).
SQ   SEQUENCE   193 AA;  21830 MW;  206E814C823E3B2E CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 193;
  Best Local Similarity   45.5%;  Pred. No. 14;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              |:|:||  : |
Db        173 RSVIYPNKLIK 183


RESULT 6
SYE_ARCFU
ID   SYE_ARCFU      STANDARD;      PRT;   551 AA.
AC   O29979;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE   (GluRS).
GN   GLTX OR AF0260.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC   Archaeoglobaceae; Archaeoglobus.
OX   NCBI_TaxID=2234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98049343; PubMed=9389475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulphate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC       diphosphate + L-glutamyl-tRNA(Glu).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AE001087; AAB90966.1; -.
DR   HSSP; P00962; 1GTR.
DR   TIGR; AF0260; -.
DR   InterPro; IPR004526; GltX_arch.
DR   InterPro; IPR000924; Glu_tRNA-synt_1c.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00749; tRNA-synt_1c; 1.
DR   PRINTS; PR00987; TRNASYNTHGLU.
DR   TIGRFAMs; TIGR00463; gltX_arch; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW   Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW   Complete proteome.
FT   SITE        100    110       "HIGH" REGION.
SQ   SEQUENCE   551 AA;  64402 MW;  A985A300C6B68F2E CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 551;
  Best Local Similarity   66.7%;  Pred. No. 41;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              |||||: |:
Db        270 VVYPTLDFE 278


RESULT 7
YKP3_KLULA
ID   YKP3_KLULA     STANDARD;      PRT;   594 AA.
AC   P05469;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Hypothetical killer plasmid PGKL-2 protein 3.
OS   Kluyveromyces lactis (Yeast).
OG   Plasmid pGKl-2.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX   NCBI_TaxID=28985;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140;
RX   MEDLINE=88289339; PubMed=3041369;
RA   Tommasino S., Ricci S., Galeotti C.L.;
RT   "Genome organization of the killer plasmid pGKL2 from Kluyveromyces
RT   lactis.";
RL   Nucleic Acids Res. 16:5863-5878(1988).
CC   -!- FUNCTION: THE PRESENCE OF THE TWO LINEAR PLASMIDS, TERMED
CC       PGKL1 AND PGKL2, IN STRAINS OF KLUYVEROMYCES LACTIS CONFERS
CC       THE KILLER PHENOTYPE TO THE HOST CELL, BY PROMOTING THE
CC       SECRETION OF A TOXIN ABLE TO INHIBIT THE GROWTH OF SENSITIVE
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CC       STRAINS.
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CC   ---------------------------------------------------------------------
DR   EMBL; X07776; CAA30604.1; -.
DR   PIR; S00961; S00961.
DR   InterPro; IPR000977; DNA_ligase.
DR   Pfam; PF01068; DNA_ligase; 1.
KW   Hypothetical protein; Plasmid.
SQ   SEQUENCE   594 AA;  70527 MW;  6AE57D37618BE6B0 CRC64;

  Query Match             56.9%;  Score 33;  DB 1;  Length 594;
  Best Local Similarity   36.4%;  Pred. No. 45;
  Matches    4;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              |: :||:::|:
Db         80 RSTMYPSLIFR 90


RESULT 8
PSBK_ORYSA
ID   PSBK_ORYSA     STANDARD;      PRT;    61 AA.
AC   P12162;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Photosystem II reaction center protein K precursor (PSII-K).
GN   PSBK.
OS   Oryza sativa (Rice).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RX   MEDLINE=89364698; PubMed=2770692;
RA   Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA   Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA   Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura M.;
RT   "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT   intermolecular recombination between distinct tRNA genes accounts for
RT   a major plastid DNA inversion during the evolution of the cereals.";
RL   Mol. Gen. Genet. 217:185-194(1989).
CC   -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
CC       OF PHOTOSYSTEM II.
CC   -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X15901; CAA34010.1; -.
DR   PIR; JQ0203; F2RZKS.
DR   InterPro; IPR003687; PSII_PsbK.
DR   Pfam; PF02533; PsbK; 1.
KW   Photosystem II; Chloroplast.
FT   PROPEP          1      24       POTENTIAL.
FT   CHAIN          25      61       PHOTOSYSTEM II REACTION CENTER PROTEIN K.
SQ   SEQUENCE   61 AA;  6982 MW;  BBC361067C4158F5 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 61;
  Best Local Similarity   55.6%;  Pred. No. 6.9;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              :|:|||  |
Db         14 SVIYPTSFF 22


RESULT 9
PSBK_WHEAT
ID   PSBK_WHEAT     STANDARD;      PRT;    61 AA.
AC   P58273;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Photosystem II reaction center protein K precursor (PSII-K).
GN   PSBK.
OS   Triticum aestivum (Wheat).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Chinese Spring;
RA   Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shiina T.,
RA   Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
RA   Gojobori T., Murai R., Murai K., Matsuoka Y., Ohnishi Y., Tajiri H.,
RA   Tsunewaki K.;
RT   "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
RT   complete sequence and contig clones.";
RL   Plant Mol. Biol. Rep. 18:243-253(2000).
CC   -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTION CENTER
CC       OF PHOTOSYSTEM II.
CC   -!- SIMILARITY: BELONGS TO THE PSBK FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB042240; BAB47017.1; -.
DR   InterPro; IPR003687; PSII_PsbK.
DR   Pfam; PF02533; PsbK; 1.
KW   Photosystem II; Chloroplast.
FT   PROPEP          1      24       BY SIMILARITY.
FT   CHAIN          25      61       PHOTOSYSTEM II REACTION CENTER PROTEIN K.
SQ   SEQUENCE   61 AA;  7030 MW;  467901067C4158FD CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 61;
  Best Local Similarity   55.6%;  Pred. No. 6.9;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              :|:|||  |
Db         14 SVIYPTSFF 22


RESULT 10
B701_HSV6G
ID   B701_HSV6G     STANDARD;      PRT;   143 AA.
AC   P30024;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Transcriptional regulatory protein B701.
OS   Human herpesvirus (type 6 / strain GS) (HHV6).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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OC   Betaherpesvirinae; Roseolovirus.
OX   NCBI_TaxID=10369;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92148942; PubMed=1310766;
RA   Geng Y., Chandran B., Josephs S.F., Wood C.;
RT   "Identification and characterization of a human herpesvirus 6 gene
RT   segment that trans activates the human immunodeficiency virus type 1
RT   promoter.";
RL   J. Virol. 66:1564-1570(1992).
CC   -!- FUNCTION: MAY BE RESPONSIBLE FOR MOST OF THE TRANS-ACTIVATING
CC       ACTIVITY ON THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROMOTER BY
CC       HHV-6. IT MAY FUNCTION BY DIRECTLY BINDING TO THE NF-KAPPAB
CC       SITE OR MAY INVOLVE CELLULAR FACTORS, SUCH AS NF-KAPPAB, EITHER
CC       DIRECTLY OR INDIRECTLY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M81789; -; NOT_ANNOTATED_CDS.
DR   PIR; A42186; WMBE6H.
KW   Transcription regulation; Trans-acting factor; Activator.
SQ   SEQUENCE   143 AA;  16385 MW;  D0CE4D7C2422AAD8 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 143;
  Best Local Similarity   50.0%;  Pred. No. 17;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :|::||  ||
Db         50 KTLLYPKTMF 59


RESULT 11
COAD_CHRVI
ID   COAD_CHRVI     STANDARD;      PRT;   169 AA.
AC   P71154;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Pantetheine-
DE   phosphate adenylyltransferase) (PPAT) (Dephospho-CoA
DE   pyrophosphorylase).
GN   COAD OR KDTB.
OS   Chromatium vinosum.
OC   Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
OC   Allochromatium.
OX   NCBI_TaxID=1049;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=D / ATCC 17899 / DSM 180;
RX   MEDLINE=96328257; PubMed=8765743;
RA   Moulis J.M.;
RT   "Molecular cloning and expression of the gene encoding Chromatium
RT   vinosum 2[4Fe-4S] ferredoxin.";
RL   Biochim. Biophys. Acta 1308:12-14(1996).
CC   -!- FUNCTION: REVERSIBLY TRANSFERS AN ADENYLYL GROUP FROM ATP TO 4'-
CC       PHOSPHOPANTETHEINE, YIELDING DEPHOSPHO-COA (DPCOA) AND
CC       PYROPHOSPHATE (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + pantetheine 4'-phosphate = diphosphate +
CC       dephospho-CoA.
CC   -!- PATHWAY: Coenzyme A (CoA) biosynthesis; fourth step.
CC   -!- SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE COAD FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U45327; AAC44332.1; -.
DR   HSSP; P23875; 1B6T.
DR   InterPro; IPR004821; Cyt_tran_rel.
DR   InterPro; IPR004820; Cytidylyltransf.
DR   InterPro; IPR001980; LPS_biosynth.
DR   Pfam; PF01467; Cytidylyltransf; 1.
DR   PRINTS; PR01020; LPSBIOSNTHSS.
DR   TIGRFAMs; TIGR00125; cyt_tran_rel; 1.
KW   Transferase; Nucleotidyltransferase; Coenzyme A biosynthesis.
SQ   SEQUENCE   169 AA;  18559 MW;  5126FD2BF32824AC CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 169;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYP 6
              ||||||
Db          2 RTVVYP 7


RESULT 12
CAKB_COTJA
ID   CAKB_COTJA     STANDARD;      PRT;   200 AA.
AC   Q98855;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Putative calcium-activated potassium channel beta subunit.
GN   CO6.
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97224079; PubMed=9070660;
RA   Oberst C., Weiskirchen R., Hartl M., Bister K.;
RT   "Suppression in transformed avian fibroblasts of a gene (CO6)
RT   encoding a membrane protein related to mammalian potassium channel
RT   regulatory subunits.";
RL   Oncogene 14:1109-1116(1997).
CC   -!- FUNCTION: POTASSIUM CHANNEL PROTEIN WHICH MAY MODULATE THE
CC       PROPERTIES OF THE PORE-FORMING ALPHA SUBUNIT (BY SIMILARITY).
CC   -!- SUBUNIT: THE CALCIUM-ACTIVATED POTASSIUM CHANNEL IS COMPOSED OF
CC       AT LEAST TWO SUBUNITS: A PORE-FORMING ALPHA SUBUNIT AND A
CC       REGULATORY BETA SUBUNIT (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U67865; AAC26967.1; -.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Ionic channel; Transmembrane; Glycoprotein.
FT   TRANSMEM     20     40       POTENTIAL.
FT   TRANSMEM    167    187       POTENTIAL.
FT   CARBOHYD     89     89       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   200 AA;  22677 MW;  B7A612D8973F711F CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 200;
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  Best Local Similarity   55.6%;  Pred. No. 23;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              | ::||:||
Db        169 TFLWPTLMF 177


RESULT 13
IP23_LYCES
ID   IP23_LYCES     STANDARD;      PRT;   201 AA.
AC   Q43502;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Proteinase inhibitor type II CEVI57 precursor.
GN   CEVI57.
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX   NCBI_TaxID=4081;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Rutgers; TISSUE=Leaf;
RX   MEDLINE=96252900; PubMed=8672818;
RA   Gadea J., Mayda E., Conejero V., Vera P.;
RT   "Characterization of defense-related genes ectopically expressed in
RT   viroid-infected tomato plants.";
RL   Mol. Plant Microbe Interact. 9:409-415(1996).
CC   -!- INDUCTION: BY VIROID INFECTION.
CC   -!- SIMILARITY: BELONGS TO THE POTATO TYPE II PROTEINASE INHIBITOR
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X94946; CAA64416.1; -.
DR   HSSP; P01080; 4SGB.
DR   InterPro; IPR003465; Prot_inhib.
DR   Pfam; PF02428; Prot_inhib_II; 3.
KW   Serine protease inhibitor; Repeat; Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    201       PROTEINASE INHIBITOR TYPE II CEVI57.
FT   REPEAT       27     83       1.
FT   REPEAT       84    143       2.
FT   REPEAT      144    199       3.
FT   ACT_SITE     32     33       INTERACTION WITH TRYPSIN (PROBABLE).
FT   ACT_SITE    147    148       INTERACTION WITH TRYPSIN (PROBABLE).
SQ   SEQUENCE   201 AA;  21419 MW;  A3FCAB93773D8590 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 201;
  Best Local Similarity   57.1%;  Pred. No. 23;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              :|::|||
Db        106 KTIIYPT 112


RESULT 14
Y473_TREPA
ID   Y473_TREPA     STANDARD;      PRT;   214 AA.
AC   O83486;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein TP0473.
GN   TP0473.
OS   Treponema pallidum.
OC   Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX   NCBI_TaxID=160;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nichols;
RX   MEDLINE=98332770; PubMed=9665876;
RA   Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA   Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA   Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA   Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA   McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA   Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA   Venter J.C.;
RT   "Complete genome sequence of Treponema pallidum, the syphilis
RT   spirochete.";
RL   Science 281:375-388(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001224; AAC65467.1; -.
DR   TIGR; TP0473; -.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM      4     23       POTENTIAL.
FT   TRANSMEM     35     57       POTENTIAL.
FT   TRANSMEM     67     89       POTENTIAL.
FT   TRANSMEM     96    118       POTENTIAL.
FT   TRANSMEM    128    150       POTENTIAL.
FT   TRANSMEM    155    177       POTENTIAL.
FT   TRANSMEM    187    209       POTENTIAL.
SQ   SEQUENCE   214 AA;  24001 MW;  1497AA7E15DFAE92 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 214;
  Best Local Similarity   66.7%;  Pred. No. 25;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMM 9
              ||||| :|:
Db        186 RTVVYTSML 194


RESULT 15
GLTT_BACCA
ID   GLTT_BACCA     STANDARD;      PRT;   421 AA.
AC   P24944;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier
DE   protein).
GN   GLTT.
OS   Bacillus caldotenax.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1395;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93062018; PubMed=1359385;
RA   Tolner B., Poolman B., Konings W.N.;
RT   "Characterization and functional expression in Escherichia coli of
RT   the sodium/proton/glutamate symport proteins of Bacillus
RT   stearothermophilus and Bacillus caldotenax.";
RL   Mol. Microbiol. 6:2845-2856(1992).
CC   -!- FUNCTION: THIS CARRIER PROTEIN IS PART OF THE NA(+)-DEPENDENT,
CC       BINDING-PROTEIN-INDEPENDENT GLUTAMATE-ASPARTATE TRANSPORT SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
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CC   -!- SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
CC       (SDF, TC 2.A.23).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M86509; AAA22493.1; -.
DR   PIR; S26246; S26246.
DR   InterPro; IPR001991; Na/diCO_symp.
DR   Pfam; PF00375; SDF; 1.
DR   PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; 1.
DR   PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; 1.
KW   Transport; Transmembrane; Symport.
FT   DOMAIN        1      3       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      4     24       POTENTIAL.
FT   DOMAIN       25     43       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     44     64       POTENTIAL.
FT   DOMAIN       65     77       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     78     98       POTENTIAL.
FT   DOMAIN       99    148       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    149    169       POTENTIAL.
FT   DOMAIN      170    198       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    199    219       POTENTIAL.
FT   DOMAIN      220    222       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    223    243       POTENTIAL.
FT   DOMAIN      244    244       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    245    265       POTENTIAL.
FT   DOMAIN      266    306       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    307    327       POTENTIAL.
FT   DOMAIN      328    330       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    331    351       POTENTIAL.
FT   TRANSMEM    352    372       POTENTIAL.
FT   DOMAIN      373    421       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   421 AA;  45345 MW;  10ABBE12EDD1E7E4 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 421;
  Best Local Similarity   75.0%;  Pred. No. 50;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              ||| ||:|
Db        226 VVYATMLF 233


RESULT 16
VAS1_BOVIN
ID   VAS1_BOVIN     STANDARD;      PRT;   468 AA.
AC   P40682;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Vacuolar ATP synthase subunit S1 precursor (EC 3.6.3.14) (V-ATPase S1
DE   subunit) (V-ATPase S1 accessory protein) (V-ATPase Ac45 subunit).
GN   ATP6IP1 OR ATP6S1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 378-388.
RC   TISSUE=Adrenal chromaffin;
RX   MEDLINE=95014142; PubMed=7929063;
RA   Supek F., Supekova L., Mandiyan S., Pan Y.-C.E., Nelson H., Nelson N.;
RT   "A novel accessory subunit for vacuolar H(+)-ATPase from chromaffin
RT   granules.";
RL   J. Biol. Chem. 269:24102-24106(1994).
CC   -!- FUNCTION: VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY
CC       OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
CC   -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC       H(+)(Out).
CC   -!- SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U10039; AAA50752.1; -.
KW   ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
KW   Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    468       VACUOLAR ATP SYNTHASE SUBUNIT S1.
FT   TRANSMEM    418    438       POTENTIAL.
FT   CARBOHYD    167    167       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    258    258       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    271    271       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    294    294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    355    355       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    404    404       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   468 AA;  51781 MW;  BF2C42D56ABB1B6D CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 468;
  Best Local Similarity   87.5%;  Pred. No. 56;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTM 8
              |||| |||
Db        244 RTVVPPTM 251


RESULT 17
TRPE_ARATH
ID   TRPE_ARATH     STANDARD;      PRT;   595 AA.
AC   P32068;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Anthranilate synthase component I-1, chloroplast precursor
DE   (EC 4.1.3.27).
GN   ASA1 OR AT5G05730 OR MJJ3.14.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93005721; PubMed=1392592;
RA   Niyogi K.K., Fink G.R.;
RT   "Two anthranilate synthase genes in Arabidopsis: defense-related
RT   regulation of the tryptophan pathway.";
RL   Plant Cell 4:721-733(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=97471969; PubMed=9330910;
RA   Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA   Miyajima N., Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT   features of the 1.6 Mb regions covered by twenty physically assigned
RT   P1 clones.";
RL   DNA Res. 4:215-230(1997).
CC   -!- CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate +
CC       pyruvate + L-glutamate.
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CC   -!- PATHWAY: Tryptophan biosynthesis; first step.
CC   -!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II.
CC   -!- SUBCELLULAR LOCATION: Chloroplast (Probable).
CC   -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
CC       USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
CC       GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M92353; AAA32738.1; -.
DR   EMBL; AB005237; BAB09667.1; -.
DR   PIR; S27751; S27751.
DR   HSSP; Q06128; 1QDL.
DR   InterPro; IPR005256; Anth_synthI.
DR   InterPro; IPR000350; Chorismate_bind.
DR   Pfam; PF00425; chorismate_bind; 1.
DR   PRINTS; PR00095; ANTSNTHASEI.
DR   ProDom; PD000779; Chorismate_bind; 1.
DR   TIGRFAMs; TIGR00564; trpE_most; 1.
KW   Tryptophan biosynthesis; Lyase; Chloroplast; Transit peptide;
KW   Multigene family.
FT   TRANSIT       1      ?       CHLOROPLAST (POTENTIAL).
FT   CHAIN         ?    595       ANTHRANILATE SYNTHASE COMPONENT I-1.
SQ   SEQUENCE   595 AA;  66311 MW;  674175416A2726F0 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 595;
  Best Local Similarity   71.4%;  Pred. No. 72;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|:|| 
Db        526 RTIVFPT 532


RESULT 18
NU5M_HYLLA
ID   NU5M_HYLLA     STANDARD;      PRT;   603 AA.
AC   P03919;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
GN   MTND5 OR ND5 OR NADH5.
OS   Hylobates lar (Common gibbon).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9580;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ester;
RA   Arnason U., Gullberg A., Xu X.;
RT   "A complete mitochondrial DNA molecule of the white-handed gibbon,
RT   Hylobates lar, and comparison among individual mitochondrial genes of
RT   all hominoid genera.";
RL   Hereditas 124:185-189(1996).
RN   [2]
RP   SEQUENCE OF 1-79 FROM N.A.
RX   MEDLINE=82242101; PubMed=6284948;
RA   Brown W.M., Prager E.M., Wang A., Wilson A.C.;
RT   "Mitochondrial DNA sequences of primates: tempo and mode of
RT   evolution.";
RL   J. Mol. Evol. 18:225-239(1982).
CC   -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X99256; CAA67638.1; -.
DR   EMBL; V00659; CAA24025.1; -.
DR   PIR; A00449; A00449.
DR   InterPro; IPR003916; NADHub_oxred5.
DR   InterPro; IPR001750; Oxidored_q1.
DR   InterPro; IPR001516; Oxidored_q1_N.
DR   Pfam; PF00361; oxidored_q1; 1.
DR   Pfam; PF00662; oxidored_q1_N; 1.
DR   PRINTS; PR01434; NADHDHGNASE5.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ   SEQUENCE   603 AA;  67360 MW;  3BFF99C6EA7BCE70 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 603;
  Best Local Similarity   71.4%;  Pred. No. 73;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 VYPTMMF 10
              ::|||||
Db         48 LFPTMMF 54


RESULT 19
RPOC_TREPA
ID   RPOC_TREPA     STANDARD;      PRT;  1416 AA.
AC   O83270;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE   beta' chain) (RNA polymerase beta' subunit).
GN   RPOC OR TP0242.
OS   Treponema pallidum.
OC   Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX   NCBI_TaxID=160;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nichols;
RX   MEDLINE=98332770; PubMed=9665876;
RA   Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA   Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA   Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA   Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA   McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA   Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA   Venter J.C.;
RT   "Complete genome sequence of Treponema pallidum, the syphilis
RT   spirochete.";
RL   Science 281:375-388(1998).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC       ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC       BETA' CHAIN.
CC   -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AE001205; AAC65230.1; -.
DR   HSSP; Q9KWU6; 1HQM.
DR   TIGR; TP0242; -.
DR   InterPro; IPR000722; RNA_pol_A.
DR   InterPro; IPR002879; RNA_pol_A2.
DR   Pfam; PF00623; RNA_pol_A; 1.
DR   Pfam; PF01854; RNA_pol_A2; 2.
KW   Transferase; DNA-directed RNA polymerase; Transcription;
KW   Complete proteome.
SQ   SEQUENCE   1416 AA;  159789 MW;  78D0EB6A1CAF7C9C CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 1416;
  Best Local Similarity   71.4%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPT 7
              ||:|||:
Db        486 RTIVYPS 492


RESULT 20
RPA1_RAT
ID   RPA1_RAT       STANDARD;      PRT;  1716 AA.
AC   O54889;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DNA-directed RNA polymerase I largest subunit (EC 2.7.7.6) (RNA
DE   polymerase I 194 kDa subunit) (RPA194).
GN   POLR1A OR RPO1-4 OR RPA1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98086309; PubMed=9422795;
RA   Hannan R.D., Hempel W.M., Cavanaugh A., Arino T., Dimitrov S.I.,
RA   Moss T., Rothblum L.;
RT   "Affinity purification of mammalian RNA polymerase I. Identification
RT   of an associated kinase.";
RL   J. Biol. Chem. 273:1257-1267(1998).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES. RNA POLYMERASE I IS ESSENTIALLY USED TO TRANSCRIBE
CC       RIBOSOMAL DNA UNITS.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 14
CC       DIFFERENT POLYPEPTIDES. THIS SUBUNIT IS THE LARGEST COMPONENT OF
CC       RNA POLYMERASE I.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
CC       FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
CC       PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
CC       III FOR 5S AND TRNA GENES.
CC   -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF025425; AAB94601.1; -.
DR   InterPro; IPR000722; RNA_pol_A.
DR   InterPro; IPR002879; RNA_pol_A2.
DR   Pfam; PF00623; RNA_pol_A; 1.
DR   Pfam; PF01854; RNA_pol_A2; 2.
KW   Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
KW   Zinc-finger; Nuclear protein.
FT   ZN_FING      64     80       C2H2-TYPE (POTENTIAL).
SQ   SEQUENCE   1716 AA;  194191 MW;  E8EE15BC23E60941 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 1716;
  Best Local Similarity   50.0%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |: || |: |
Db        224 TITYPAMVHK 233


RESULT 21
RPOA_EAV
ID   RPOA_EAV       STANDARD;      PRT;  3175 AA.
AC   P19811; Q88625;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   POL polyprotein (ORF1A/1B) [Contains: RNA-directed RNA polymerase
DE   (EC 2.7.7.48); Helicase; Protease (EC 3.4.21.-)].
GN   POL.
OS   Equine arteritis virus (EAV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC   Arteriviridae; Arterivirus.
OX   NCBI_TaxID=11047;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bucyrus;
RX   MEDLINE=91237805; PubMed=1851863;
RA   den Boon J.A., Snijder E.J., Chirnside E.D., de Vries A.A.F.,
RA   Horzinek M.C., Spaan W.J.M.;
RT   "Equine arteritis virus is not a togavirus but belongs to the
RT   coronaviruslike superfamily.";
RL   J. Virol. 65:2910-2920(1991).
RN   [2]
RP   SEQUENCE OF 1-17 FROM N.A.
RC   STRAIN=Bucyrus;
RX   MEDLINE=90287699; PubMed=2162519;
RA   de Vries A.A.F., Chirnside E.D., Bredenbeek P.J., Gravestein L.A.,
RA   Horzinek M.C., Spaan W.J.M.;
RT   "All subgenomic mRNAs of equine arteritis virus contain a common
RT   leader sequence.";
RL   Nucleic Acids Res. 18:3241-3247(1990).
CC   -!- FUNCTION: RNA-DIRECTED RNA POLYMERASE & POSSIBLE HELICASE. A
CC       ROLE FOR NTP-BINDING PROTEINS IN RNA DUPLEX UNWINDING HAS BEEN
CC       SUGGESTED. ALSO CONTAINS A PROTEASE DOMAIN.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- MISCELLANEOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
CC       FOR 1727-ASN AND 1728-LEU.
CC   -!- SIMILARITY: WITH THE POLYMERASE PROTEIN OF OTHER CORONAVIRUSES AND
CC       OF TOROVIRUSES.
CC   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S32.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X53459; CAA37539.1; ALT_SEQ.
DR   EMBL; X53459; CAA37540.1; ALT_SEQ.
DR   EMBL; X52277; CAA36520.1; -.
DR   PIR; S10158; S10158.
DR   PIR; A39925; RRWVEV.
DR   MEROPS; C31.UNW; -.
DR   MEROPS; C32.001; -.
DR   MEROPS; C33.001; -.
DR   MEROPS; S32.001; -.
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DR   InterPro; IPR000606; Viral_helicase1.
DR   Pfam; PF01443; Viral_helicase1; 1.
KW   RNA-directed RNA polymerase; Transferase; Helicase; ATP-binding;
KW   Hydrolase; Serine protease; Zinc-finger.
FT   CHAIN         1   1727       ORF1A.
FT   CHAIN      1728   3175       ORF1B.
FT   DOMAIN     1080   1220       TRYPSIN-LIKE SERINE PROTEASE.
FT   DOMAIN     1218   1506       HELICASE.
FT   DOMAIN     2098   2306       POLYMERASE.
FT   ACT_SITE   1103   1103       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   1129   1129       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   1184   1184       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ZN_FING    2368   2414       BY SIMILARITY.
FT   NP_BIND    2528   2535       ATP (BY SIMILARITY).
SQ   SEQUENCE   3175 AA;  345275 MW;  ED5C8BA0E31DE695 CRC64;

  Query Match             55.2%;  Score 32;  DB 1;  Length 3175;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 YPTMMF 10
              ||||:|
Db       1369 YPTMLF 1374


RESULT 22
SMP1_HUMAN
ID   SMP1_HUMAN     STANDARD;      PRT;   157 AA.
AC   O95807;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Small membrane protein 1.
GN   SMP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hu G.;
RT   "A new member of the 18 kDa small membrane protein family in human.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21154917; PubMed=11230166;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a catalog of human genes and proteins: sequencing and
RT   analysis of 500 novel complete protein coding human cDNAs.";
RL   Genome Res. 11:422-435(2001).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANT VAL-58.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA   Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: STRONG, TO C21ORF4.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF081282; AAD17754.1; -.
DR   EMBL; AL136627; CAB66562.1; -.
DR   EMBL; AF458851; AAL51108.1; -.
DR   MIM; 605348; -.
KW   Transmembrane; Polymorphism.
FT   TRANSMEM     26     46       POTENTIAL.
FT   TRANSMEM     58     78       POTENTIAL.
FT   TRANSMEM     95    115       POTENTIAL.
FT   TRANSMEM    126    146       POTENTIAL.
FT   VARIANT      58     58       A -> V.
FT                                /FTId=VAR_013121.
FT   VARIANT     141    141       F -> L.
FT                                /FTId=VAR_007851.
SQ   SEQUENCE   157 AA;  17400 MW;  8CDF83AA23EBB1FA CRC64;

  Query Match             53.4%;  Score 31;  DB 1;  Length 157;
  Best Local Similarity   83.3%;  Pred. No. 29;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 VVYPTM 8
              |:||||
Db         44 VIYPTM 49


RESULT 23
YQJI_ECOLI
ID   YQJI_ECOLI     STANDARD;      PRT;   207 AA.
AC   Q46872;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein yqjI.
GN   YQJI OR B3071.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U28379; AAA89150.1; -.
DR   EMBL; AE000389; AAC76106.1; -.
DR   EcoGene; EG12954; yqjI.
DR   InterPro; IPR005149; PadR.
DR   Pfam; PF03551; PadR; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   207 AA;  23401 MW;  DD3D108D83E087F7 CRC64;

  Query Match             53.4%;  Score 31;  DB 1;  Length 207;
  Best Local Similarity   62.5%;  Pred. No. 39;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              |:|||: |
Db         99 VIYPTLDF 106


RESULT 24
DNC_HUMAN
```

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ID   DNC_HUMAN      STANDARD;      PRT;   320 AA.
AC   Q9HC21;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling
DE   protein 1).
GN   SLC25A19 OR DNC OR MUP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   PubMed=11226231;
RA   Dolce V., Fiermonte G., Runswick M.J., Palmieri F., Walker J.E.;
RT   "The human mitochondrial deoxynucleotide carrier and its role in the
RT   toxicity of nucleoside antivirals.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Renard S., Mondesert G., Besnard F.;
RT   "MUP 1, a mitochondrial uncoupling protein.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Responsible for the uptake of deoxynucleotides into the
CC       matrix of the mitochondria. Transports all four deoxy NDPs, and,
CC       less efficiently, the corresponding dNTPs. Does not transport
CC       dNMPs, NMPs, deoxynucleosides, nucleosides, purines, or
CC       pyrimidines. Supply deoxynucleotides to the mitochondrial matrix
CC       for conversion to triphosphates and incorporation into
CC       mitochondrial DNA.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC       inner membrane.
CC   -!- TISSUE SPECIFICITY: Expressed in all tissues examined except for
CC       placenta. Highest levels in colon, kidney, lung, testis, spleen,
CC       and brain.
CC   -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC   -!- DISEASE: Likely to be medically important by providing the means
CC       of uptake into mitochondria of nucleoside analogs, leading to the
CC       mitochondrial impairment that underlies the toxic side effects of
CC       such drugs in the treatment of viral illnesses, including AIDS,
CC       and in cancer therapy.
CC   -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ251857; CAC27560.1; -.
DR   EMBL; AJ301616; CAC37793.1; -.
DR   EMBL; AF182404; AAG16903.1; -.
DR   EMBL; BC001075; AAH01075.1; -.
DR   EMBL; BC005120; AAH05120.1; -.
DR   Genew; HGNC:14409; SLC25A19.
DR   MIM; 606521; -.
DR   InterPro; IPR002067; Mit_carrier.
DR   InterPro; IPR001993; Mitoch_carrier.
DR   Pfam; PF00153; mito_carr; 3.
DR   PRINTS; PR00926; MITOCARRIER.
DR   PROSITE; PS00215; MITOCH_CARRIER; 2.
KW   Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT   TRANSMEM     19     39       POTENTIAL.
FT   TRANSMEM     87    107       POTENTIAL.
FT   TRANSMEM    122    142       POTENTIAL.
FT   TRANSMEM    173    193       POTENTIAL.
FT   TRANSMEM    293    313       POTENTIAL.
SQ   SEQUENCE   320 AA;  35511 MW;  57CE0F01D538B1BE CRC64;

  Query Match             53.4%;  Score 31;  DB 1;  Length 320;
  Best Local Similarity   45.5%;  Pred. No. 61;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              :|: ||  :||
Db        231 KTLTYPLDLFK 241


RESULT 25
MSP1_YEAST
ID   MSP1_YEAST     STANDARD;      PRT;   362 AA.
AC   P28737;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   MSP1 protein (TAT-binding homolog 4).
GN   MSP1 OR YTA4 OR YGR028W.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SF747-19D;
RX   MEDLINE=94043260; PubMed=8226973;
RA   Nakai M., Endo T., Hase T., Matsubara H.;
RT   "Intramitochondrial protein sorting. Isolation and characterization
RT   of the yeast MSP1 gene which belongs to a novel family of putative
RT   ATPases.";
RL   J. Biol. Chem. 268:24262-24269(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RX   MEDLINE=95274317; PubMed=7754704;
RA   Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehnle S.,
RA   Schwarzlose C., Vetter I., Feldmann H.;
RT   "Identification of a set of yeast genes coding for a novel family of
RT   putative ATPases with high similarity to constituents of the 26S
RT   protease complex.";
RL   Yeast 10:1141-1155(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RX   MEDLINE=97435481; PubMed=9290212;
RA   Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
RT   "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
RT   chromosome VII.";
RL   Yeast 13:1077-1090(1997).
RN   [4]
RP   SEQUENCE OF 280-362 FROM N.A.
RC   STRAIN=SC167;
RX   MEDLINE=92204135; PubMed=1552903;
RA   Lisowsky T.;
RT   "Dual function of a new nuclear gene for oxidative phosphorylation
RT   and vegetative growth in yeast.";
RL   Mol. Gen. Genet. 232:58-64(1992).
CC   -!- FUNCTION: INVOLVED IN INTRAMITOCHONDRIAL SORTING OF PROTEINS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC       outer membrane.
CC   -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; X68055; CAA48191.1; -.
DR   EMBL; X81069; CAA56956.1; -.
DR   EMBL; Z72813; CAA97015.1; -.
DR   EMBL; X60722; -; NOT_ANNOTATED_CDS.
DR   PIR; S20468; S20468.
DR   PIR; S37410; S37410.
DR   SGD; S0003260; MSP1.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003959; AAA_ATPase_centr.
DR   InterPro; IPR003960; AAA_sub.
DR   Pfam; PF00004; AAA; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00674; AAA; 1.
KW   ATP-binding; Mitochondrion; Outer membrane; Transmembrane.
FT   DOMAIN        1     12       INTERMEMBRANE (POTENTIAL).
FT   TRANSMEM     13     28       POTENTIAL.
FT   DOMAIN       29    362       CYTOPLASMIC (POTENTIAL).
FT   NP_BIND     133    140       ATP (POTENTIAL).
SQ   SEQUENCE   362 AA;  40343 MW;  1B3562A32F47F434 CRC64;

  Query Match             53.4%;  Score 31;  DB 1;  Length 362;
  Best Local Similarity   62.5%;  Pred. No. 69;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMM 9
              :|:|| ||
Db        106 SVIYPLMM 113


Search completed: July 16, 2003, 14:35:16
Job time : 11.3333 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 14:30:45 ; Search time 41.6667 Seconds
(without alignments)
54.396 Million cell updates/sec

Title: US-09-923-716C-4
Perfect score: 58
Sequence: 1 RTVVYPTMMFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	70.7	333	16	Q55184	Q55184 synechocyst
2	41	70.7	974	5	O01574	O01574 caenorhabdi
3	38	65.5	394	16	Q9CIU3	Q9ciu3 lactococcus
4	37	63.8	390	10	Q8VWX1	Q8vwx1 perilla fru
5	37	63.8	391	10	Q9ZPP7	Q9zpp7 perilla fru
6	37	63.8	395	16	Q9I2X4	Q9i2x4 pseudomonas
7	36	62.1	512	10	Q9LUC5	Q9luc5 arabidopsis
8	35	60.3	180	10	Q9FX69	Q9fx69 arabidopsis
9	35	60.3	254	10	Q93ZC5	Q93zc5 arabidopsis
10	35	60.3	258	10	Q9LS01	Q9ls01 arabidopsis
11	35	60.3	264	16	Q8ZLZ1	Q8zlz1 salmonella
12	35	60.3	282	10	Q94JV3	Q94jv3 arabidopsis
13	35	60.3	320	11	Q8VGS2	Q8vgs2 mus musculu
14	35	60.3	435	16	Q9WZI6	Q9wzi6 thermotoga
15	35	60.3	504	12	Q9EME6	Q9eme6 amsacta moo
16	35	60.3	598	16	Q8Z3N6	Q8z3n6 salmonella
17	35	60.3	705	5	Q8SWA5	Q8swa5 encephalito
18	35	60.3	733	10	Q8S7E2	Q8s7e2 oryza sativ
19	35	60.3	735	10	Q9FJR9	Q9fjr9 arabidopsis
20	35	60.3	887	10	Q9ZVV2	Q9zvv2 arabidopsis
21	35	60.3	1030	3	Q9HFQ9	Q9hfq9 emericella
22	34	58.6	54	12	Q84121	Q84121 influenzavi
23	34	58.6	173	13	Q8UUZ6	Q8uuz6 brachydanio
24	34	58.6	180	16	Q98ID0	Q98id0 rhizobium l
25	34	58.6	212	16	Q8XNC4	Q8xnc4 clostridium
26	34	58.6	217	17	Q9HHU4	Q9hhu4 halobacteri
27	34	58.6	303	10	O64685	O64685 arabidopsis
28	34	58.6	316	10	Q9LSV4	Q9lsv4 arabidopsis
29	34	58.6	320	17	Q8U223	Q8u223 pyrococcus
30	34	58.6	322	4	Q96LB2	Q96lb2 homo sapien
31	34	58.6	322	4	Q8TDD9	Q8tdd9 homo sapien
32	34	58.6	322	4	Q8TDD8	Q8tdd8 homo sapien
33	34	58.6	347	2	Q9KIS7	Q9kis7 brucella ab
34	34	58.6	347	16	Q8YDZ2	Q8ydz2 brucella me
35	34	58.6	373	2	P95523	P95523 photobacter
36	34	58.6	373	2	Q52100	Q52100 photobacter
37	34	58.6	389	16	Q8ZA85	Q8za85 yersinia pe
38	34	58.6	404	16	Q8Z2F8	Q8z2f8 salmonella
39	34	58.6	464	10	Q9LEW3	Q9lew3 arabidopsis
40	34	58.6	530	17	Q973Z9	Q973z9 sulfolobus
41	34	58.6	674	16	Q9WZS4	Q9wzs4 thermotoga
42	34	58.6	711	10	Q9C8R8	Q9c8r8 arabidopsis
43	33.5	57.8	1304	5	O96959	O96959 drosophila
44	33.5	57.8	1508	5	Q8T049	Q8t049 drosophila
45	33.5	57.8	1724	5	O96960	O96960 drosophila
46	33.5	57.8	1752	5	Q9U4K9	Q9u4k9 drosophila
47	33.5	57.8	1810	5	Q9V483	Q9v483 drosophila
48	33	56.9	120	16	O31535	O31535 bacillus su
49	33	56.9	159	8	Q950X8	Q950x8 tetrahymena
50	33	56.9	205	2	Q51516	Q51516 pseudomonas
51	33	56.9	205	16	Q9HUC4	Q9huc4 pseudomonas
52	33	56.9	221	16	Q8ZDB7	Q8zdb7 yersinia pe
53	33	56.9	237	10	Q8RX02	Q8rx02 arabidopsis
54	33	56.9	261	10	Q9SUW6	Q9suw6 arabidopsis
55	33	56.9	299	4	Q9NXA8	Q9nxa8 homo sapien
56	33	56.9	310	4	Q9Y6E6	Q9y6e6 homo sapien
57	33	56.9	390	16	Q8YFX4	Q8yfx4 brucella me
58	33	56.9	457	17	Q9HLH0	Q9hlh0 thermoplasm
59	33	56.9	457	17	Q978Q5	Q978q5 thermoplasm
60	33	56.9	474	10	Q43541	Q43541 lilium long
61	33	56.9	531	17	Q97V62	Q97v62 sulfolobus
62	33	56.9	703	12	Q83467	Q83467 porcine ade
63	33	56.9	725	5	Q9VD08	Q9vd08 drosophila
64	33	56.9	821	16	Q9RXG4	Q9rxg4 deinococcus
65	33	56.9	842	17	Q970B4	Q970b4 sulfolobus
66	33	56.9	1021	5	O15733	O15733 dictyosteli
67	33	56.9	1063	4	Q8TDZ7	Q8tdz7 homo sapien
68	33	56.9	1235	16	Q929A9	Q929a9 listeria in
69	33	56.9	1235	16	Q8Y511	Q8y511 listeria mo
70	33	56.9	1824	5	Q9U0Y5	Q9u0y5 leishmania
71	32	55.2	61	10	Q8S6G8	Q8s6g8 oryza sativ
72	32	55.2	132	8	Q956K0	Q956k0 rhodotorula
73	32	55.2	136	16	Q8XFN0	Q8xfn0 salmonella
74	32	55.2	143	12	Q9WT48	Q9wt48 human herpe
75	32	55.2	143	12	Q9DYD9	Q9dyd9 human herpe

ALIGNMENTS

RESULT 1
Q55184
ID Q55184 PRELIMINARY; PRT; 333 AA.
AC Q55184;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein sll0456.
GN SLL0456.

```
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX   NCBI_TaxID=1148;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC 6803;
RA   Tabata S.;
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96127529; PubMed=8590279;
RA   Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA   Sugiura M., Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT   region from map positions 64% to 92% of the genome.";
RL   DNA Res. 2:153-166(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97061201; PubMed=8905231;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA   Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA   Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
DR   EMBL; D64001; BAA10324.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   333 AA;  37436 MW;  676E7399E4499ED6 CRC64;

  Query Match             70.7%;  Score 41;  DB 16;  Length 333;
  Best Local Similarity   77.8%;  Pred. No. 6.5;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              ||||||::|
Db        172 TVVYPTLVF 180


RESULT 2
O01574
ID   O01574      PRELIMINARY;      PRT;   974 AA.
AC   O01574;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 111.6 kDa protein.
GN   F48C1.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Gattung S., Le T.T.;
RT   "The sequence of C. elegans cosmid F48C1.";
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U97015; AAB52345.1; -.
DR   InterPro; IPR000602; Glyco_hydro_38.
DR   Pfam; PF01074; Glyco_hydro_38; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   974 AA;  111586 MW;  C825EFA33FB2F964 CRC64;

  Query Match             70.7%;  Score 41;  DB 5;  Length 974;
  Best Local Similarity   60.0%;  Pred. No. 18;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              :|::|| |||
Db        851 QTIIYPPMMF 860


RESULT 3
Q9CIU3
ID   Q9CIU3      PRELIMINARY;      PRT;   394 AA.
AC   Q9CIU3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   ABC transporter ATP binding protein.
GN   YCGB OR LL0263.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC   Streptococcaceae; Lactococcus.
OX   NCBI_TaxID=1360;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
DR   EMBL; AE006263; AAK04361.1; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR001140; ABCtranprtrTM.
DR   InterPro; IPR003439; ABC_transportr.
DR   Pfam; PF00664; ABC_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transportr; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   394 AA;  43946 MW;  2822CBC28AEA4C36 CRC64;

  Query Match             65.5%;  Score 38;  DB 16;  Length 394;
  Best Local Similarity   66.7%;  Pred. No. 29;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              |::|||| |
Db         47 TLIYPTMRF 55


RESULT 4
Q8VWX1
ID   Q8VWX1      PRELIMINARY;      PRT;   390 AA.
AC   Q8VWX1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Delta-15 desaturase.
GN   FAD3.
OS   Perilla frutescens.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
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OX   NCBI_TaxID=48386;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. OKDONG; TISSUE=DEVELOPING SEED;
RA   Kim K.-H., Hwang S.-K., Hwang Y.-S.;
RT   "Cloning of Perilla delta-15 desaturase.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF213482; AAL36934.1; -.
DR   InterPro; IPR001225; FA_desaturase.
DR   Pfam; PF00487; FA_desaturase; 1.
DR   ProDom; PD001081; FA_desaturase; 2.
SQ   SEQUENCE   390 AA;  44857 MW;  6959C941D47A15AB CRC64;

  Query Match             63.8%;  Score 37;  DB 10;  Length 390;
  Best Local Similarity   70.0%;  Pred. No. 44;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |:| | ||||
Db        241 TIVGPNMMFK 250


RESULT 5
Q9ZPP7
ID   Q9ZPP7      PRELIMINARY;      PRT;   391 AA.
AC   Q9ZPP7;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Omega-3 fatty acid desaturase.
GN   FAD3.
OS   Perilla frutescens.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
OX   NCBI_TaxID=48386;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. SUWON-8;
RX   MEDLINE=99205707; PubMed=10189709;
RA   Chung C.-H., Kim J.-L., Lee Y.-C., Choi Y.-L.;
RT   "Cloning and characterization of a seed-specific omega-3 fatty acid
RT   desaturase cDNA from Perilla frutescens.";
RL   Plant Cell Physiol. 40:114-118(1999).
DR   EMBL; AF047039; AAD15744.1; -.
DR   InterPro; IPR001225; FA_desaturase.
DR   Pfam; PF00487; FA_desaturase; 1.
DR   ProDom; PD001081; FA_desaturase; 2.
SQ   SEQUENCE   391 AA;  44931 MW;  6637E81654C17CEC CRC64;

  Query Match             63.8%;  Score 37;  DB 10;  Length 391;
  Best Local Similarity   70.0%;  Pred. No. 45;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              |:| | ||||
Db        242 TIVGPNMMFK 251


RESULT 6
Q9I2X4
ID   Q9I2X4      PRELIMINARY;      PRT;   395 AA.
AC   Q9I2X4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Hypothetical protein PA1765.
GN   PA1765.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
DR   EMBL; AE004602; AAG05154.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   395 AA;  44670 MW;  FC183A433B2529C8 CRC64;

  Query Match             63.8%;  Score 37;  DB 16;  Length 395;
  Best Local Similarity   60.0%;  Pred. No. 45;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | ||||:::|
Db        292 RQVVYPSLLF 301


RESULT 7
Q9LUC5
ID   Q9LUC5      PRELIMINARY;      PRT;   512 AA.
AC   Q9LUC5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Cytochrome P450 (Putative cytochrome P450 protein).
GN   MIE1.20.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RA   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=20277480; PubMed=10819329;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT   features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT   clones.";
RL   DNA Res. 7:131-135(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA   Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA   Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA   Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA   Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
RA   Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA   Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA   Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT   "Full Length cDNA of gene MIE1.20 (GI:9294391).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR   EMBL; AB023038; BAB02401.1; -.
DR   EMBL; AY050827; AAK92762.1; -.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00385; P450.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   512 AA;  58442 MW;  19DDEEAD9C9BAF0B CRC64;
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  Query Match             62.1%;  Score 36;  DB 10;  Length 512;
  Best Local Similarity   63.6%;  Pred. No. 90;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | | ||  |||
Db         80 RVVPYPLQMFK 90


RESULT 8
Q9FX69
ID   Q9FX69      PRELIMINARY;      PRT;   180 AA.
AC   Q9FX69;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   T6J4.4 protein.
GN   T6J4.4.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA   Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
RA   Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA   Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
RA   Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC011810; AAG09557.1; -.
SQ   SEQUENCE   180 AA;  19794 MW;  5DA0943DB333F332 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 180;
  Best Local Similarity   60.0%;  Pred. No. 51;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        124 RQLVYPTKLF 133


RESULT 9
Q93ZC5
ID   Q93ZC5      PRELIMINARY;      PRT;   254 AA.
AC   Q93ZC5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   At1g13280/T6J4_23.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA   Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA   Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA   Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA   Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA   Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA   Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA   Ecker J.R.;
RT   "Arabidopsis cDNA clones.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY057636; AAL15267.1; -.
SQ   SEQUENCE   254 AA;  27809 MW;  4D82FA4889242353 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 254;
  Best Local Similarity   60.0%;  Pred. No. 72;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        198 RQLVYPTKLF 207


RESULT 10
Q9LS01
ID   Q9LS01      PRELIMINARY;      PRT;   258 AA.
AC   Q9LS01;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Genomic DNA, chromosome 3, TAC clone:K13N2.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RA   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=20277480; PubMed=10819329;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT   features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT   clones.";
RL   DNA Res. 7:131-135(2000).
DR   EMBL; AB028607; BAA95765.1; -.
SQ   SEQUENCE   258 AA;  28398 MW;  42AF942E0E9AAB87 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 258;
  Best Local Similarity   60.0%;  Pred. No. 73;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | :|||| :|
Db        202 RQLVYPTKLF 211


RESULT 11
Q8ZLZ1
ID   Q8ZLZ1      PRELIMINARY;      PRT;   264 AA.
AC   Q8ZLZ1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative arylsulfate sulfotransferase.
GN   STM3192.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
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RL   Nature 413:852-856(2001).
DR   EMBL; AE008846; AAL22066.1; -.
KW   Transferase; Hypothetical protein; Complete proteome.
SQ   SEQUENCE   264 AA;  29462 MW;  2B3F39791813620F CRC64;

  Query Match             60.3%;  Score 35;  DB 16;  Length 264;
  Best Local Similarity   66.7%;  Pred. No. 74;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              :|:|| |||
Db        256 LVHPTQMFK 264


RESULT 12
Q94JV3
ID   Q94JV3      PRELIMINARY;      PRT;   282 AA.
AC   Q94JV3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   AT5g46920/MQD22_6.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA   Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA   Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA   Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
RA   Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA   Davis R.W., Theologis A., Ecker J.R.;
RT   "Arabidopsis cDNA clones.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF372919; AAK49635.1; -.
DR   InterPro; IPR000442; Intron_maturse2.
DR   Pfam; PF01348; Intron_maturas2; 1.
SQ   SEQUENCE   282 AA;  32875 MW;  89B0C6FFA2ABF4B8 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 282;
  Best Local Similarity   60.0%;  Pred. No. 79;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |||||: :
Db          9 RRVVYPTLRY 18


RESULT 13
Q8VGS2
ID   Q8VGS2      PRELIMINARY;      PRT;   320 AA.
AC   Q8VGS2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Olfactory receptor MOR187-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073074; AAL60737.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   320 AA;  36768 MW;  1FF2EBF1413280F1 CRC64;

  Query Match             60.3%;  Score 35;  DB 11;  Length 320;
  Best Local Similarity   75.0%;  Pred. No. 89;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMM 9
              ||:|| ||
Db         82 TVIYPKMM 89


RESULT 14
Q9WZI6
ID   Q9WZI6      PRELIMINARY;      PRT;   435 AA.
AC   Q9WZI6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PMBA-related protein.
GN   TM0727.
OS   Thermotoga maritima.
OC   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX   NCBI_TaxID=2336;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MSB8 / DSM 3109;
RX   MEDLINE=99287316; PubMed=10360571;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA   Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
DR   EMBL; AE001743; AAD35809.1; -.
DR   TIGR; TM0727; -.
DR   InterPro; IPR002510; PmbA_TldD.
DR   Pfam; PF01523; PmbA_TldD; 1.
KW   Complete proteome.
SQ   SEQUENCE   435 AA;  48306 MW;  C8764A342A975819 CRC64;

  Query Match             60.3%;  Score 35;  DB 16;  Length 435;
  Best Local Similarity   54.5%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMFK 11
              | |: ||:|:|
Db        135 RVVMVPTVMYK 145


RESULT 15
Q9EME6
ID   Q9EME6      PRELIMINARY;      PRT;   504 AA.
AC   Q9EME6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   AMV260.
GN   AMV260.
OS   Amsacta moorei entomopoxvirus (AmEPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC   Entomopoxvirus B.
OX   NCBI_TaxID=28321;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RX   MEDLINE=20396580; PubMed=10936094;
RA   Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
RA   Moyer R.W.;
RT   "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
RT   Analysis and Comparison with Other Poxviruses.";
RL   Virology 274:120-139(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
RA   Moyer R.W.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF250284; AAG02966.1; -.
SQ   SEQUENCE   504 AA;  61862 MW;  ACA9BFFA559FAA50 CRC64;

  Query Match             60.3%;  Score 35;  DB 12;  Length 504;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              ||::|:::|:
Db        459 TVIFPSLLFR 468


RESULT 16
Q8Z3N6
ID   Q8Z3N6      PRELIMINARY;      PRT;   598 AA.
AC   Q8Z3N6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Probable arylsulfate sulfotransferase.
GN   STY3370.
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
DR   EMBL; AL627278; CAD07717.1; -.
KW   Transferase; Complete proteome.
SQ   SEQUENCE   598 AA;  66586 MW;  B5434F028A5421F0 CRC64;

  Query Match             60.3%;  Score 35;  DB 16;  Length 598;
  Best Local Similarity   66.7%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMFK 11
              :|:|| |||
Db        590 LVHPTQMFK 598


RESULT 17
Q8SWA5
ID   Q8SWA5      PRELIMINARY;      PRT;   705 AA.
AC   Q8SWA5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein ECU02_1230.
GN   ECU02_1230.
OS   Encephalitozoon cuniculi.
OC   Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX   NCBI_TaxID=6035;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GB-M1;
RA   Genoscope;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GB-M1;
RX   MEDLINE=21576510; PubMed=11719806;
RA   Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA   Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
RA   Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA   Weissenbach J., Vivares C.P.;
RT   "Genome sequence and gene compaction of the eukaryote parasite
RT   Encephalitozoon cuniculi.";
RL   Nature 414:450-453(2001).
DR   EMBL; AL590442; CAD25152.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   705 AA;  79649 MW;  235B834A40258AEF CRC64;

  Query Match             60.3%;  Score 35;  DB 5;  Length 705;
  Best Local Similarity   62.5%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMM 9
              ||:|||::
Db        570 TVIYPTLL 577


RESULT 18
Q8S7E2
ID   Q8S7E2      PRELIMINARY;      PRT;   733 AA.
AC   Q8S7E2;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 82.3 kDa protein.
GN   OSJNBA0057L21.15.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA   Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA   Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
RA   VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA   Salzberg S.L., White O., Fraser C.M.;
RT   "Oryza sativa chromosome 10 BAC OSJNBa0057L21 genomic sequence.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC087599; AAL79699.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   733 AA;  82297 MW;  24C8521E18220D9D CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 733;
  Best Local Similarity   60.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |||||: :
Db        462 RRVVYPTLRY 471


RESULT 19
Q9FJR9
ID   Q9FJR9      PRELIMINARY;      PRT;   735 AA.
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AC   Q9FJR9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Similarity to maturase-related protein.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=98403884; PubMed=9734815;
RA   Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA   Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT   Sequence features of the regions of 1,367,185 bp covered by 19
RT   physically assigned P1 and TAC clones.";
RL   DNA Res. 5:203-216(1998).
DR   EMBL; AB013394; BAB10231.1; -.
DR   InterPro; IPR000442; Intron_maturse2.
DR   InterPro; IPR000477; RVTse.
DR   Pfam; PF01348; Intron_maturas2; 1.
DR   Pfam; PF00078; rvt; 1.
KW   RNA-directed DNA polymerase.
SQ   SEQUENCE   735 AA;  85179 MW;  3C4A940CDA6E1590 CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 735;
  Best Local Similarity   60.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              | |||||: :
Db        462 RRVVYPTLRY 471


RESULT 20
Q9ZVV2
ID   Q9ZVV2      PRELIMINARY;      PRT;   887 AA.
AC   Q9ZVV2;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   T5A14.3 protein.
GN   T5A14.3.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA   Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA   Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA   Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC005223; AAD10640.1; -.
DR   HSSP; P17119; 3KAR.
DR   InterPro; IPR001752; kinesin_motor.
DR   Pfam; PF00225; kinesin; 1.
DR   PRINTS; PR00380; KINESINHEAVY.
DR   SMART; SM00129; KISc; 1.
DR   PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW   ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ   SEQUENCE   887 AA;  99904 MW;  748B215B02E2E9BC CRC64;

  Query Match             60.3%;  Score 35;  DB 10;  Length 887;
  Best Local Similarity   70.0%;  Pred. No. 2.4e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMFK 11
              ||| ||:| |
Db        696 TVVNPTLMLK 705


RESULT 21
Q9HFQ9
ID   Q9HFQ9      PRELIMINARY;      PRT;  1030 AA.
AC   Q9HFQ9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chitinase.
GN   CHIC.
OS   Emericella nidulans (Aspergillus nidulans).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=5072;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FGSC 4;
RA   Specht C.A., Benfield B.B., Garcia J.J.;
RT   "Identification of bacteria-like chitinases in fungi.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF314225; AAG34171.1; -.
DR   HSSP; P10968; 2CWG.
DR   InterPro; IPR001579; Chitinase_18/2.
DR   InterPro; IPR001002; Chitin_binding_1.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   Pfam; PF00187; Chitin_bind_1; 1.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   ProDom; PD000471; Glyco_hydro_18; 1.
DR   ProDom; PD000609; Chitin_binding_1; 1.
DR   SMART; SM00270; ChtBD1; 2.
DR   PROSITE; PS01095; CHITINASE_18; 1.
DR   PROSITE; PS00026; CHITIN_BINDING; 1.
KW   Chitin-binding.
SQ   SEQUENCE   1030 AA;  112748 MW;  8EE1E64192AF03E5 CRC64;

  Query Match             60.3%;  Score 35;  DB 3;  Length 1030;
  Best Local Similarity   66.7%;  Pred. No. 2.7e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TVVYPTMMF 10
              || |||: |
Db        951 TVTYPTLTF 959


RESULT 22
Q84121
ID   Q84121      PRELIMINARY;      PRT;    54 AA.
AC   Q84121;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Influenza A/Shearwater/Australia/75 (H5N3), neuraminidase (Seg 6), 5'
DE   end (Fragment).
OS   Influenzavirus A.
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenza A viruses.
OX   NCBI_TaxID=11320;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83017869; PubMed=6927853;
RA   Blok J., Air G.M.;
RT   "Sequence variation at the 3' end of the neuraminidase gene from 39
RT   influenza type A viruses.";
RL   Virology 121:211-229(1982).
DR   EMBL; K01014; AAA43416.1; -.
DR   InterPro; IPR001860; GH_34.
DR   Pfam; PF00064; neur; 1.
FT   NON_TER      54      54
SQ   SEQUENCE   54 AA;  5916 MW;  B0BD49BBF05D0153 CRC64;
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  Query Match           58.6%;  Score 34;  DB 12;  Length 54;
  Best Local Similarity  75.0%;  Pred. No. 25;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTM 8
              :|||||||:
Db         43 QTVVYPTI 50


RESULT 23
Q8UUZ6
ID   Q8UUZ6      PRELIMINARY;      PRT;   173 AA.
AC   Q8UUZ6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Alpha A crystallin.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LENS;
RA   Runkle S., Hill J., Kantorow M., Horwitz J., Posner M.;
RT   "Cloning and characterization of zebrafish (Danio rerio) alpha A-
RT   crystallin.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY035778; AAK61363.1; -.
DR   InterPro; IPR001436; Crystallin_alpha.
DR   InterPro; IPR003090; Crystallin_N.
DR   InterPro; IPR002068; Hsp20.
DR   Pfam; PF00525; crystallin; 1.
DR   Pfam; PF00011; HSP20; 1.
DR   PRINTS; PR00299; ACRYSTALLIN.
DR   ProDom; PD001193; Crystallin_N; 1.
DR   PROSITE; PS01031; HSP20; 1.
SQ   SEQUENCE   173 AA;  19714 MW;  301D743DB91BBC13 CRC64;

  Query Match           58.6%;  Score 34;  DB 13;  Length 173;
  Best Local Similarity  60.0%;  Pred. No. 77;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RTVVYPTMMF 10
              ||: ||| :|
Db         12 RTLGYPTRLF 21


RESULT 24
Q98ID0
ID   Q98ID0      PRELIMINARY;      PRT;   180 AA.
AC   Q98ID0;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein mll2459.
GN   MLL2459.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
DR   EMBL; AP002999; BAB49586.1; -.
DR   InterPro; IPR005149; PadR.
DR   Pfam; PF03551; PadR; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   180 AA;  19909 MW;  D94F736B2855CF60 CRC64;

  Query Match           58.6%;  Score 34;  DB 16;  Length 180;
  Best Local Similarity  75.0%;  Pred. No. 80;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 VVYPTMMF 10
              |||||: |
Db         49 VVYPTLTF 56


RESULT 25
Q8XNC4
ID   Q8XNC4      PRELIMINARY;      PRT;   212 AA.
AC   Q8XNC4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein CPE0414.
GN   CPE0414.
OS   Clostridium perfringens.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC   Clostridiales; Clostridiaceae; Clostridium.
OX   NCBI_TaxID=1502;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=13 / TYPE A;
RX   PubMed=11792842;
RA   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA   Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT   "Complete genome sequence of Clostridium perfringens, an anaerobic
RT   flesh-eater.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR   EMBL; AP003186; BAB80120.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   212 AA;  24363 MW;  DB7E1E2AC94BE697 CRC64;

  Query Match           58.6%;  Score 34;  DB 16;  Length 212;
  Best Local Similarity  62.5%;  Pred. No. 94;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 VYPTMMFK 11
              :|| |:||
Db        205 IYPNMIFK 212


Search completed: July 16, 2003, 14:37:07
Job time : 42 secs
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